

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:33:52 : Search time 35 Seconds

(without alignments)  
921.333 Million cell updates/sec

Title: US-09-981-087a-2

Perfect score: 1218

Sequence: 1 MGRGRVQLKRENNKINQVT.....LTPNSILPAMMLPTTNE 242

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A.GeneSeq\_101002:\*

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- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1218	100.0	242	20	AAW80998 Arabidopsis AGL8-1
2	1218	100.0	242	20	AAW89921 Arabidopsis AGL8 p
3	1218	100.0	242	21	AAAG28304 Arabidopsis thalia
4	909	74.6	180	21	AAAG28305 Arabidopsis thalia
5	753	61.8	246	20	AAW95018 petunia MADS box
6	742.5	61.0	242	21	AAAB32574 Eucalyptus grandis
7	734.5	60.3	244	17	AAAR99634 Eucalyptus SOE-1 p
8	734.5	60.1	245	17	AAAR99636 Eucalyptus SOE-2L
9	707.5	58.1	205	17	AAAR99635 Eucalyptus SOE-2S
10	669.5	55.0	262	21	AAV69920 MADS box protein.

11	662.5	54.4	255	18	AAW23811
12	662.5	54.4	255	20	AAW67571
13	662.5	54.4	256	19	AAW3109
14	662.5	54.4	256	19	AAW39131
15	662.5	54.4	256	19	AAW43326
16	662.5	54.4	256	21	AAAG52893
17	662.5	54.4	256	21	AAAG4912
18	662.5	54.4	256	21	AAV67550
19	662.5	54.4	256	21	AAV78880
20	662.5	54.4	300	21	AAAB19241
21	662.5	54.4	302	19	AAW69327
22	661.5	54.3	256	21	AAAG17300
23	660	54.2	245	22	AAW50265
24	654	53.7	253	19	AAW69329
25	654	53.7	253	19	AAW3110
26	654	53.7	253	19	AAW39132
27	654	53.7	253	19	AAW43327
28	654	53.7	253	21	AAAB19242
29	654	53.7	253	21	AAV67551
30	654	53.7	253	21	AAV78881
31	653	53.6	130	21	AAAG28306
32	648	53.2	253	18	AAW23812
33	647	53.1	255	18	AAW23813
34	647	53.1	255	19	AAW69330
35	647	53.1	255	19	AAW43111
36	647	53.1	255	19	AAW43328
37	647	53.1	255	19	AAW39133
38	647	53.1	255	21	AAAB19243
39	647	53.1	255	21	AAV67552
40	647	53.1	255	21	AAV78882
41	627	51.5	255	18	AAW23815
42	627	51.5	255	19	AAW69324
43	627	51.5	255	19	AAW43113
44	627	51.5	255	19	AAW39135
45	627	51.5	255	19	AAW43330

#### ALIGNMENTS

RESULT 1  
AAW80998 standard; Protein: 242 AA.

AAW80998:

10-MAY-1999 (first entry)

Arabidopsis AGL8-like gene product.

AGL8-like gene product; agamous-like 8 gene; transcription factor;  
seed dispersal; dehiscence; transgenic plant.

Arabidopsis thaliana.

W09900502-A1.

07-JAN-1999.

25-JUN-1998; 98W0-US13208.

28-APR-1998; 98US-0067800.

27-JUN-1997; 97US-0051030.

(RECG ) UNIV CALIFORNIA.

Ferrandiz C, Yanofsky MF;  
WPI: 1999-095747/08.

N-PSDB; AAV99856.

Use of agamous-like nucleic acids - useful for the production of  
transgenic seed plants in which dehiscence is modified resulting in

PT delayed seed dispersal  
XX  
XX  
PS Claim 3; Fig 6; 126pp; English.  
XX

This is the deduced amino acid sequence of the Arabidopsis agamous-like 8 (AGL8) gene product. AGL8 is a transcription factor that regulates dehiscence. The invention provides a transgenic seed plant that is characterised by delayed seed dispersal due to ectopic expression of a nucleic acid molecule (see AAV99856) encoding an AGL8-like gene product. The ectopically expressed nucleic acid molecule may be operatively linked to an exogenous regulatory element such as a dehiscence zone-selective regulatory element derived from the Arabidopsis AGL1 gene (see AAV99857) or AGL5 gene (see AAV99858). The transgenic seed plants include members of the Brassicaceae, such as rapeseed, and members of the Fabaceae, such as soybean, pea, lentil and bean. A plant expression vector comprising a dehiscence zone-selective regulatory element, and a kit for producing the transgenic seed plants are also provided.

XX  
SQ Sequence 242 AA;

Query Match 100.0%; Score 1218; DB 20; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.1e-99;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 SCMERILEYDRLYSDKOLVGRDVSQSENWVLEHAKLKARVEVLEKKNRMFGEDLSL 120  
DB 61 SCMERILEYDRLYSDKOLVGRDVSQSENWVLEHAKLKARVEVLEKKNRMFGEDLSL 120  
QY 121 SLEKLSLEHOLDAAIKTSIRSRKNQAMFESISALQKKDKALQDHNNSLTKIKEREKKTG 180  
DB 121 SLEKLSLEHOLDAAIKTSIRSRKNQAMFESISALQKKDKALQDHNNSLTKIKEREKKTG 180  
QY 181 QOEGOLVQCSNSSSVLLPQYCVTSSRDGFVERVGENGASSLTEPNSLLPAMMLRPTTT 240  
DB 181 QOEGOLVQCSNSSSVLLPQYCVTSSRDGFVERVGENGASSLTEPNSLLPAMMLRPTTT 240  
QY 241 NE 242  
DB 241 NE 242

RESULT 2

AAW98921  
ID AAW98921 standard; Protein; 242 AA.

XX  
AC AAW98921;  
XX  
DT 06-MAY-1999 (first entry)  
XX  
DE Arabidopsis AGL8 protein sequence.  
XX  
KW Arabidopsis; AGL8; agamous-like 8; seed plant; fruit size.  
XX  
OS Arabidopsis sp.  
XX  
PN MO9900503-A1.  
XX  
PD 07-JAN-1999.  
XX  
PF 26-JUN-1998; 98MO-US13249.  
XX  
PR 27-JUN-1997; 97US-0051030.  
XX  
PA (COLD- ) COLD SPRING HARBOR LAB.  
XX  
PI (REGC ) UNIV CALIFORNIA.  
XX  
PI Ferrandiz C, Gu Q, Martienssen R, Yanofsky MF;  
XX

DR WPI; 1999-095748/08.  
DR N-PSDB; AAX18594.  
XX

PT use of agamous-like 8 related nucleic acids - useful for producing  
PT transgenic seed plants which can produce seed or fruit of increased  
PT or decreased size  
XX

PS Claim 3; Fig 1; 68pp; English.  
XX

The present invention describes a non-naturally occurring seed plant comprising an ectopically expressed nucleic acid molecule encoding an agamous-like 8 (AGL8)-related gene product. The seed plant characterised by producing seeds of increased size. The present sequence represents Arabidopsis AGL-8. The seed plant can be used for producing seed or fruit of increased or decreased size. The present invention can relate to seed plants such as, e.g. canola, soybean, pea, broad bean, peanut, coconut, sunflower, cotton, coffee, cacao, citrus, grape, apples, strawberry, olive and tomato.

XX  
SQ Sequence 242 AA;

Query Match 100.0%; Score 1218; DB 20; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.1e-99;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGVQLKRIENKINROYTFSKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
DB 1 MGRGVQLKRIENKINROYTFSKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
QY 61 SCMERILEYDRLYSDKOLVGRDVSQSENWVLEHAKLKARVEVLEKKNRMFGEDLSL 120  
DB 61 SCMERILEYDRLYSDKOLVGRDVSQSENWVLEHAKLKARVEVLEKKNRMFGEDLSL 120  
QY 121 SLEKLSLEHOLDAAIKTSIRSRKNQAMFESISALQKKDKALQDHNNSLTKIKEREKKTG 180  
DB 121 SLEKLSLEHOLDAAIKTSIRSRKNQAMFESISALQKKDKALQDHNNSLTKIKEREKKTG 180  
QY 181 QOEGOLVQCSNSSSVLLPQYCVTSSRDGFVERVGENGASSLTEPNSLLPAMMLRPTTT 240  
DB 181 QOEGOLVQCSNSSSVLLPQYCVTSSRDGFVERVGENGASSLTEPNSLLPAMMLRPTTT 240  
QY 241 NE 242  
DB 241 NE 242

RESULT 3

AAG28304  
ID AAG28304 standard; Protein; 242 AA.

XX  
AC AAG28304;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33471.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130044.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
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PR 11-MAY-1999; 99US-0132865.  
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Query Match 100.0%; Score 1218; DB 21; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.1e-99;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGRGVQLKRIKINRQYTFKRRSGLLKKAHEISVLCDAEVALYFSSKGLFEKSTG 60  
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DB 121 SLEKQSLLEHQLDAIKSIRSRKNQMFESISALQKKDVALODHNSLLKIKEREKKTG 180  
OY 181 QOEGQLVQCSNSSSVLLPQYCTSSRDGFEVERGGENGASSLTERNSLLPAMMLRPTTT 240  
DB 181 QOEGQLVQCSNSSSVLLPQYCTSSRDGFEVERGGENGASSLTERNSLLPAMMLRPTTT 240  
OY 241 NE 242  
DB 241 NE 242

RESULT 4  
AAG28305  
ID AAG28305 standard; Protein: 180 AA.  
XX

AC AAG28305;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 33472.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.

XX Arabidopsis thaliana.

OS  
XX  
XX  
PN  
XX+  
EPI033405-A2.

1

PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
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PR 05-MAR-1999; 9905-0123180.  
PR 09-MAR-1999; 9905-0123548.  
PR 23-MAR-1999; 9905-0125788.  
PR 25-MAR-1999; 9905-0126264.  
PR 29-MAR-1999; 9905-0126785.  
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PR 21-MAY-1999; 9905-0135353.  
PR 24-MAY-1999; 9905-0135629.  
PR 25-MAY-1999; 9905-0136021.  
PR 27-MAY-1999; 9905-0136392.  
PR 28-MAY-1999; 9905-0136782.  
PR 01-JUN-1999; 9905-0137222.  
PR 03-JUN-1999; 9905-0137528.  
PR 04-JUN-1999; 9905-0137502.  
PR 07-JUN-1999; 9905-0137724.  
PR 08-JUN-1999; 9905-0138094.  
PR 10-JUN-1999; 9905-0138540.  
PR 10-JUN-1999; 9905-0138847.  
PR 14-JUN-1999; 9905-0139119.  
PR 16-JUN-1999; 9905-0139452.  
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PR 17-JUN-1999; 9905-0139492.  
PR 18-JUN-1999; 9905-0139454.  
PR 18-JUN-1999; 9905-0139455.  
PR 18-JUN-1999; 9905-0139456.  
PR 18-JUN-1999; 9905-0139457.  
PR 18-JUN-1999; 9905-0139458.  
PR 18-JUN-1999; 9905-0139459.  
PR 18-JUN-1999; 9905-0139460.  
PR 18-JUN-1999; 9905-0139461.  
PR 18-JUN-1999; 9905-0139462.  
PR 18-JUN-1999; 9905-0139463.  
PR 18-JUN-1999; 9905-0139750.  
PR 18-JUN-1999; 9905-0139763.  
PR 21-JUN-1999; 9905-0139817.  
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PR 23-JUN-1999; 9905-0140354.  
PR 24-JUN-1999; 9905-0140695.  
PR 28-JUN-1999; 9905-0140823.  
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PR 30-JUN-1999; 9905-0141287.  
PR 01-JUL-1999; 9905-0141842.  
PR 01-JUL-1999; 9905-0142154.  
PR 02-JUL-1999; 9905-0142055.



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PR 06-JUL-1999; 99US-0142390.
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PR 09-JUL-1999; 99US-0142920.
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PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149902.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 22-SEP-1999; 99US-0155139.

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PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
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PR 18-OCT-1999; 99US-0159584.
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PR 21-OCT-1999; 99US-0160768.
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PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 74.6%; Score 909; DB 21; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.6e-72;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 MERTLEPRDRYIXSKQVGRVYVSOSENNVLEHAKIKARVEVLEKKNRPFKEDDLSL 122
DB 1 MERTLEPRDRYIXSKQVGRVYVSOSENNVLEHAKIKARVEVLEKKNRPFKEDDLSL 60
QY 123 KELOSLEHOLDIAIKSIRSRKQAMPESTISALOKKDKALODHNNLSLKKIKREKKTGOO 182
DB 61 KELOSLEHOLDIAIKSIRSRKQAMPESTISALOKKDKALODHNNLSLKKIKREKKTGOO 120
QY 183 EGOIVQCSNSSSVLLPQYCVTSSRDGFVERVGVGENGAGASLTPNSLIPAMMLRPTTNE 242
DB 121 EGOIVQCSNSSSVLLPQYCVTSSRDGFVERVGVGENGAGASLTPNSLIPAMMLRPTTNE 180

RESULT 5
AAM95018
ID AAM95018 standard; Protein: 246 AA.
AC AAM95018;
DE 21-MAY-1999 (first entry)
DT 21-MAY-1999 (first entry)
DX Petunia MADS box transcription factor, FBp10.
DE Petunia MADS box transcription factor, FBp10.
KW Petunia; MADS box; transcription factor; FBp10; flowering; inhibition;
KW inflorescence; vegetative organ; storage organ; wood production;
KW nitrogen fixation; ornamental plant.
OS Petunia sp.
XX
XX Key Location/Qualifiers
FH
```

FT Region 1..56 /note="MADS box region"  
XX  
XX WO9904003-A1.  
XX  
XX 28-JAN-1999.  
XX  
XX 18-JUL-1997; 97WO-NL00424.  
XX  
XX 18-JUL-1997; 97WO-NL00424.  
XX  
XX (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.  
XX  
XX Angenent GC, Busscher M, Franken J;  
XX  
XX WPI; 1999-132247/11.  
XX  
XX N-PSDB; AAX17796.  
XX  
XX New DNA sequence encoding a MADS box transcription factor, FBPI0 -  
XX  
XX useful for producing transgenic plants in which flowering is  
XX  
XX inhibited  
XX  
XX Claim 1; Fig 1; 38pp; English.  
XX  
XX  
XX This represents a petunia MADS box transcription factor, FBPI0 protein.  
XX  
XX This can be used in a process of producing a transgenic plant in which  
XX  
XX flowering is inhibited due to the expression of endogenous FBPI0 or a  
XX  
XX homologous gene being inhibited; This is useful for producing plants  
XX  
XX without inflorescences or flowers which is beneficial for directing the  
XX  
XX high energy, which seeds and flowers utilize, to form vegetative organs  
XX  
XX or deposition in storage organs. Therefore, the total biomass of  
XX  
XX vegetative tissues such as roots, tubers, stem and leaves can be  
XX  
XX increased. This is particularly useful for plants used economically e.g.  
XX  
XX lettuce, spinach, chicory, sugar beet, potato, trees for wood production,  
XX  
XX tobacco, grasses, plants for nitrogen fixation, ornamental plants for  
XX  
XX production of cuttings.  
XX  
XX  
XX Sequence 246 AA:  
SQ  
Query Match 61.8%; Score 753; DB 20; Length 246;  
Best Local Similarity 63.1%; Pred. No. 1.5e-58;  
Matches 157; Conservative 34; Mismatches 38; Indels 20; Gaps 4;  
QY 1 MGRGVOLKRIENKINROYTFKRRSGLLKKAHEISVLCDAEVALIVFSKGLFEYSTD 60  
Db 1 MGRGVOMKRIENKINROYTFKRRSGLLKKAHEISVLCDAEVALIVFSKGLFEYSTD 60  
QY 61 SCMERILEYRYDRLYSKOLVGRDVSQSENWVLEHAFLKARVELEKKNRNFGEEDLSL 120  
Db 61 SCMERILEYRYEYSAERQVSTDHSSPGSWNLEHAFLKARIEVQVRNRHMGEDLSL 120  
QY 121 SKELOSLHEQDAAIKSIRSRKNQAMFESISALOKKDALODHNSLLKRIKEREKKTG 180  
Db 121 SMKDLONEQDQDSSILKHSRKNQAMFESISALOKKDALODHNSLLKRIKEREKKTG 180  
QY 181 Q-----QEGQVQCNSSSVLLPQ-----YCVTSSNDGFPERVGENGAGSLTEPR 227  
Db 181 QOTQEQDQNHHEINSSSEVLPQPLDSPHLEAVYSTVD-----NGEVEGASQ-QOPA 233  
QY 228 SLTPAMMLR 236  
Db 234 NTMPFWMMLR 242  
RESULT 6  
ID AAB32574  
XX AAB32574 standard; Protein: 242 AA.  
AC  
XX AAB32574:  
XX  
XX 25-JAN-2001 (first entry)  
XX  
XX Eucalyptus grandis transcription factor protein sequence #32.  
DE

XX plant; transcription factor; gene expression; eucalyptus; pine; acacia;  
XX poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;  
XX basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;  
XX homeodomain zipper; LIM domain; AP2; ERBS; zinc finger domain;  
XX type 2 Cys2His2; CCAAT box element; MYB.  
XX  
XX Eucalyptus grandis.  
XX  
XX WO200053724-A2.  
XX  
XX 14-SEP-2000.  
XX  
XX 09-MAR-2000; 2000WO-US06112.  
XX  
XX 11-MAR-1999; 99US-0266513.  
XX  
XX 18-AUG-1999; 99US-0149485.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
XX Wood M, McGrath A, Shenk MA, Glenn M;  
XX  
XX WPI; 2000-579369/54.  
XX  
XX  
XX New isolated polynucleotide encoding a plant transcription factor for  
XX  
XX producing a plant e.g. a woody plant, preferably eucalyptus or pine,  
XX  
XX having modified gene expression or modified activity of a polypeptide  
XX  
XX  
XX Claim 8; Page 211; 747pp; English.  
XX  
XX  
XX The present invention relates to novel plant transcription factors from  
XX  
XX Eucalyptus grandis or Pinus radiata. The present sequence is one such  
XX  
XX transcription factor. The transcription factor may be used to produce a  
XX  
XX plant having modified gene expression such as a woody plant e.g. a  
XX  
XX eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or  
XX  
XX to modify the activity of a polypeptide in a plant. The transcription  
XX  
XX factors of the present invention are members from the following families  
XX  
XX of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic  
XX  
XX helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain  
XX  
XX zipper, LIM domain, AP2 and ERBS, zinc finger domains of type 2  
XX  
XX Cys2His2, CCAAT box elements and MYB.  
XX  
XX  
XX Sequence 242 AA:  
SQ  
Query Match 61.0%; Score 742.5; DB 21; Length 242;  
Best Local Similarity 64.6%; Pred. No. 1.3e-57;  
Matches 155; Conservative 34; Mismatches 44; Indels 7; Gaps 5;  
QY 1 MGRGVOLKRIENKINROYTFKRRSGLLKKAHEISVLCDAEVALIVFSKGLFEYSTD 60  
Db 1 MGRGRLOLKRIENKINROYTFKRRAGLLKKAHEISVLCDAEVALIIFSAGKLFYEYSTD 60  
QY 61 SCMERILEYRYDRLYSKOLVGRDVSQSENWVLEHAFLKARVELEKKNRNFGEEDLSL 120  
Db 61 SCMERILEYRYEYSEHVLASSETISGWTLEHAFLKARIEVLRHVRHFMGEDLSL 120  
QY 121 SKELOSLHEQDAAIKSIRSRKNQAMFESISALOKKDALODHNSLLKRIKEREKKTG 180  
Db 121 SLKDLONEQDQDSSILKHSRKNQAMFESISALOKKDALODHNSLLKRIKEREKKTG 180  
QY 181 QOEGQVQCNS--SSVLLPQYCVTSSRDG--FVERVGENGAGSLTEP--NSLLPAMML 235  
Db 181 QO-AQWEGQDHDALDSPVVLPHYLPDLIDNGSYQARHNGHDG--ENUTOPRAGTLLPMMML 238  
RESULT 7  
ID AAR99634  
XX AAR99634 standard; Protein: 244 AA.  
AC  
XX AAR99634:  
XX  
XX

DT 01-OCT-1996 (first entry)  
XX  
XX Eucalyptus SOE-1 protein.  
XX  
XX Eucalyptus; reproductive gene; SOE-1; Arabidopsis; agamous gene;  
KW Antirrhinum; plena gene; sterility; fertility; forest tree;  
KW transgenic plant; flower development; antisense; ribozyme.  
XX  
OS Eucalyptus globulus.  
XX  
FH Key Location/Qualifiers  
FT Region 2..57  
FT /label= MADS\_box  
XX  
XX AU9539013-A.  
XX  
XX 30-MAY-1996.  
XX  
XX 22-NOV-1995; 95AU-0039013.  
XX  
XX 22-NOV-1994; 94AU-0009589.  
XX  
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX  
XX Dennis ES, Harcourt RL, Kyozeuka J, Llewellyn D;  
PI Peacock WJ, Southerton S;  
XX  
XX WPI: 1996-278411/29.  
XX  
XX N-PSDB; AAT34429.  
XX  
XX Eucalyptus reproductive genes - useful for prodn. of sterile  
PT Eucalyptus trees useful for establishing wood lot plantations or in  
PT re-forestation projects  
XX  
XX Disclosure: Page 31-32; 60pp; English.  
XX  
XX SOE-1 protein (AAR9634) is the product of a cDNA clone, SOE1  
CC (AAT34429), isolated from Eucalyptus globulus cDNA on the basis of  
CC its homology to the Arabidopsis agamous (Ag) and Antirrhinum plena  
CC (PLe) flower development gene MADS box regions. Related proteins,  
CC SOE-25 (AAR9635) and SOE-2L (AAR9636), have also been identified.  
CC Antisense or ribozyme constructs of SOE, or of PLe2 and AGE genes  
CC (see also AAT34426, AAT34428 and AAT34432), may be useful in producing  
CC sterile transgenic Eucalyptus trees by minimizing inflorescence.  
XX  
XX Sequence 244 AA:  
SQ  
Query Match 60.3%; Score 734.5; DB 17; Length 244;  
Best Local Similarity 64.4%; Pred. No. 6.6e-57;  
Matches 154; Conservative 34; Mismatches 44; Indels 7; Gaps 5;

XX  
XX 01-OCT-1996 (first entry)  
XX  
XX Eucalyptus SOE-2L protein.  
XX  
XX Eucalyptus; reproductive gene; SOE-2L; Arabidopsis; agamous gene;  
KW Antirrhinum; plena gene; sterility; fertility; forest tree;  
KW transgenic plant; flower development; antisense; ribozyme.  
XX  
XX Eucalyptus globulus.  
XX  
XX Key Location/Qualifiers  
FT Region 2..57  
FT /label= MADS\_box  
XX  
XX AU9539013-A.  
XX  
XX 30-MAY-1996.  
XX  
XX 22-NOV-1995; 95AU-0039013.  
XX  
XX 22-NOV-1994; 94AU-0009589.  
XX  
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX  
XX Dennis ES, Harcourt RL, Kyozeuka J, Llewellyn D;  
PI Peacock WJ, Southerton S;  
XX  
XX WPI: 1996-278411/29.  
XX  
XX N-PSDB; AAT34431.  
XX  
XX Eucalyptus reproductive genes - useful for prodn. of sterile  
PT Eucalyptus trees useful for establishing wood lot plantations or in  
PT re-forestation projects  
XX  
XX Disclosure: Page 36-37; 60pp; English.  
XX  
XX SOE-2L protein (AAR9636) is the product of a cDNA clone, SOE2L  
CC (AAT34431), isolated from Eucalyptus globulus cDNA on the basis of  
CC its homology to the Arabidopsis agamous (Ag) and Antirrhinum plena  
CC (PLe) flower development gene MADS box regions. Related proteins,  
CC SOE-1 (AAR9634) and SOE-2S (AAR9635), have also been identified.  
CC Antisense or ribozyme constructs of SOE, or of PLe2 and AGE genes  
CC (see also AAT34426, AAT34428 and AAT34432), may be useful in producing  
CC sterile transgenic Eucalyptus trees by minimizing inflorescence.  
XX  
XX Sequence 245 AA:  
SQ  
Query Match 60.1%; Score 732.5; DB 17; Length 245;  
Best Local Similarity 63.4%; Pred. No. 1e-56;  
Matches 156; Conservative 27; Mismatches 46; Indels 17; Gaps 4;

```

RESULT 9
AAR9635
ID AAR9635 standard; Protein; 205 AA.
XX
AC AAR9635;
XX
DT 01-OCT-1996 (first entry)
XX
DE Eucalyptus SQE-2S protein.
XX
KW Eucalyptus; reproductive gene; SQE-2S; Arabidopsis; agamous gene;
KW Antirrhinum; plena gene; sterility; fertility; forest tree;
KW transgenic plant; flower development; antisense; ribozyme.
XX
OS Eucalyptus globulus.
XX
FH Key Location/Qualifiers
FT Region 2..57
FT /label= MADS_box
XX
PN AU9539013-A.
XX
PD 30-MAY-1996.
XX
PE 22-NOV-1995; 95AU-0039013.
XX
PR 22-NOV-1994; 94AU-0009589.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI Dennis ES, Harcourt RL, Kyoizuka J, Llewellyn D;
PI Peacock WJ, Southerton S;
XX
DR WP1; 1996-278411/29.
DR N-PSDB; AAT34430.
XX
PT Eucalyptus reproductive genes - useful for prodn. of sterile
PT Eucalyptus trees useful for establishing wood lot plantations or in
PT re-forestation projects
XX
PS Disclosure; Page 34-35; 60pp; English.
XX
SQ SQE-2S protein (AAR9635) is the product of a cDNA clone, SQE2S
CC (AAT34430), isolated from Eucalyptus globulus cDNA on the basis of
CC its homology to the Arabidopsis agamous (AG) and Antirrhinum plena
CC (PLE) flower development gene MADS box regions. Related proteins,
CC SQE-1 (AAR9634) and SQE-2L (AAR9636), have also been identified.
CC Antisense or ribozyme constructs of SQE, or of FLE2 and AGE genes
CC (see also AAT34426, AAT34428 and AAT34432), may be useful in producing
CC sterile transgenic Eucalyptus trees by minimizing inflorescence.
XX
SQ Sequence 205 AA;
Query Match 58.1%; Score 707.5; DB 17; Length 205;
Best Local Similarity 70.2%; Pred. No. 1.3e-54;
Matches 144; Conservative 22; Mismatches 28; Indels 11; Gaps 2;
OY 1 MGRGVQLRIENKINROYTFSKRRSGGLKKAHEISVLCDAEVALIVFSSKGKLFESTD 60
DB 1 MGRGVQLRIENKINROYTFSKRRSGGLKKAHEISVLCDAEVALIVFSSKGKLFESTD 60
OY 61 SCMEILERYDRYLSKQOLVGRDVSQSENWVLEHAHKLKARVEVELEKRNFMGEDLDSL 120
DB 61 SCMEILERYDRYLSKQOLVGRDVSQSENWVLEHAHKLKARVEVELEKRNFMGEDLDSL 120
OY 121 SLKELOSLEHODALAIKSTRSRKNQAMFESISALOKKDALODHNNSLKIKEREKKTG 180
DB 121 SLKELOSLEHODALAIKSTRSRKNQAMFESISALOKKDALODHNNSLKIKEREKKTG 180
OY 121 SLKELOSLEHODALAIKSTRSRKNQAMFESISALOKKDALODHNNSLKIKEREKKTG 180
DB 121 SLKELOSLEHODALAIKSTRSRKNQAMFESISALOKKDALODHNNSLKIKEREKKTG 180
OY 181 QOEGQLVQCSN-----SSSVLLP 198
DB 181 QO-----TQWMDNRPQDDGLTSSSGSLP 201

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RESULT 10
AAV69920
ID AAV69920 standard; Protein; 262 AA.
XX
AC AAV69920;
XX
DT 11-APR-2000 (first entry)
XX
DE MADS box protein.
XX
KW MADS box; transcription factor; flower organ differentiation;
KW flower bud formation.
XX
OS Gentiana triflora.
XX
PN JP11346773-A.
XX
PD 21-DEC-1999.
XX
PE 10-JUN-1998; 98JP-0161895.
XX
PR 10-JUN-1998; 98JP-0161895.
XX
PA (IWATE-) IWATE KEN.
XX
DR WP1; 2000-109690/10.
DR N-PSDB; AAZ49161.
XX
PT MADS box gene coding transcription controlling factor - useful for
PT controlling the flower bud-forming period
XX
PS Claim 1; Page 7-8; 8pp; Japanese.
XX
CC This sequence is the MADS box gene protein of the invention. The
CC protein has the transcription activity of a gene participating in the
CC differentiation of flower organ. The gene controls the flower bud-forming
CC period when introduced into a plant body. The gene is useful for the
CC diversification of flowering time and height.
XX
SQ Sequence 262 AA;
Query Match 55.0%; Score 669.5; DB 21; Length 262;
Best Local Similarity 54.3%; Pred. No. 4.1e-51;
Matches 144; Conservative 36; Mismatches 50; Indels 35; Gaps 5;
OY 1 MGRGVQLRIENKINROYTFSKRRSGGLKKAHEISVLCDAEVALIVFSSKGKLFESTD 60
DB 1 MGRGVQLRIENKINROYTFSKRRSGGLKKAHEISVLCDAEVALIVFSSKGKLFESTD 60
OY 61 SCMEILERYDRYLSKQOLVGRDVSQSENWVLEHAHKLKARVEVELEKRNFMGEDLDSL 120
DB 61 SSMESILERYERYSDYDEKRIINGTESQAKDNMSMEYPKLVSRTELQXNIRHREGDLNPL 120
OY 121 SLKELOSLEHODALAIKSTRSRKNQAMFESISALOKKDALODHNNSLKIKEREKKTG 180
DB 121 NMKELOSLEHODALAIKSTRSRKNQAMFESISALOKKDALODHNNSLKIKEREKKTG 180
OY 181 QOEGQ-----IVQCSN-----SSSVLLPQ-----YCVTSSRQGFVERVNGE 216
DB 181 QOQMSADQHRVLVDVSNHPPSPPLFPQSLSIOPPLQOPEIHROT-----ETIGSD 234
OY 217 NG-----GASSLTPNSLPAWMLR 236
DB 235 GGGNGNGNGTEAAGTNTIHMPPMVNR 259

```

```

RESULT 11
AAW23811
ID AAW23811 standard; Protein; 255 AA.
XX
AC AAW23811;
XX

```

DT 11-MAY-1998 (first entry)  
 XX Arabidopsis floral meristem identity gene APETALA (AP1) product.  
 DE  
 XX  
 KM Floral meristem identity gene; APETALA1, AP1 gene;  
 KM flower development; transgenic plant; angiosperm.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN W09727287-A1.  
 XX  
 PD 31-JUL-1997.  
 PD  
 XX 26-JAN-1996; 96WO-US01041.  
 PF  
 XX 26-JAN-1996; 96WO-US01041.  
 PR  
 XX (RSGC ) UNIV CALIFORNIA.  
 PA  
 XX Yanofsky MF;  
 PI  
 XX WPI: 1997-393675/36.  
 DR N-PSDB; AAT76885 and AAT76892.  
 DR  
 XX Cauliflower floral meristem identity genes and related proteins -  
 PT used to develop products for converting shoot meristem to floral  
 PT meristem and promoting early flowering in an angiosperm  
 XX  
 XX Disclosure; Fig 1A-B; 132pp; English.  
 PS  
 XX This sequence comprises the Arabidopsis thaliana APETALA (AP1)  
 CC floral meristem identity gene product that is involved in the  
 CC conversion of shoot meristem to floral meristem. Arabidopsis AP1  
 CC cDNA and genomic DNA sequences are provided (see AAT76885 and AAT76892).  
 CC Mutation of the AP1 gene results in replacement of a few basal  
 CC flowers by inflorescence shoots that are not subtended by flowers.  
 CC When AP1 is ecotopically expressed in shoot meristem, the shoot  
 CC meristem is converted to floral meristem and early flowering can  
 CC occur. The invention relates to floral meristem identity genes  
 CC AP1, LFY and especially CAL (see AAT76885-97 and AAT9437) and gene  
 CC products (see AAM23811-18) and their use in converting shoot meristem  
 CC to floral meristem and in promoting early flowering in transgenic  
 CC plants, especially angiosperms such as cereal plants, leguminous  
 CC plants, oilseed plants, trees, fruit-bearing plants or ornamental  
 CC flowers.  
 CC  
 XX Sequence 255 AA;  
 SQ  
 Query Match 54.4%; Score 662.5; DB 18; Length 255;  
 Best Local Similarity 65.8%; Pred. No. 1.6e-50;  
 Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

QY 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
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 DB 61 SCMERILERYRYLYSKQVGRDVSQSENNVLEHAKAKARVEYLEKKRNFMGCDLSL 120  
 QY 121 SLKETQSLEHQLDAIKIRSRKNQAMFESISALOKKDKAKADHNSLTKIKEREK-KT 179  
 DB 121 SPKEQNLNEQDLTRALKIRTRKNDLMEISINELOKKAKAIOBONSMLSKOIKEREKILR 180  
 QY 180 GQQR--GGLVQCSNSSSVLLPQ 199  
 DB 181 AQQEQMDQONCGHNNPPLPQ 202

RESULT 12  
 AAM67571  
 ID AAM67571 standard; Protein: 255 AA.  
 XX

AC AAM67571;  
 XX  
 DT 02-MAR-1999 (first entry)  
 XX Arabidopsis LEAFY protein.  
 DE  
 XX Genetically modified plant; transgenic plant; flower meristem identity;  
 KM LEAFY; APETALA1; genome; flower meristem development; flowering time;  
 KM environmental condition; crop production.  
 XX  
 XX Arabidopsis thaliana.  
 XX  
 XX Key Location/Qualifiers  
 FH  
 FT Misc-difference 19  
 FT /note= "encoded by GG"  
 FT Misc-difference 39  
 FT /note= "encoded by TT"  
 FT Misc-difference 59  
 FT /note= "encoded by AT"  
 FT Misc-difference 79  
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 FT Misc-difference 99  
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 FT Misc-difference 119  
 FT /note= "encoded by GA"  
 FT Misc-difference 139  
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 FT Misc-difference 199  
 FT /note= "encoded by CG"  
 FT Misc-difference 219  
 FT /note= "encoded by TT"  
 FT Misc-difference 239  
 FT /note= "encoded by GA"  
 PN US5844119-A.  
 XX  
 XX 01-DEC-1998.  
 PD  
 XX 21-DEC-1995; 95US-0576156.  
 PF  
 XX 21-DEC-1995; 95US-0576156.  
 PR 21-DEC-1994; 94US-0360336.  
 XX  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 PI Weigel D;  
 XX  
 XX WPI: 1999-044675/04.  
 DR N-PSDB; AAV81351.  
 DR  
 XX Genetically modified plant - having in its genome a heterologous  
 PT nucleic acid sequence encoding a specified flower meristem identity  
 PT protein  
 PS  
 XX Disclosure; Column 19-22; 19pp; English.  
 XX  
 CC The invention relates to the production of a genetically modified plant  
 CC having a heterologous nucleic acid sequence encoding a flower meristem  
 CC identity protein selected from LEAFY and/or APETALA1 inserted into  
 CC its genome, which results in accelerated flower meristem development in  
 CC the plant. This sequence corresponds to the Arabidopsis thaliana LEAFY  
 CC protein, the gene for which is used in the method of the invention.  
 CC The modified plants have their flowering times controlled or induced,  
 CC regardless of locale or the environmental conditions, thus allowing the  
 CC production of crops at any given time.  
 CC  
 XX Sequence 255 AA;  
 SQ  
 Query Match 54.4%; Score 662.5; DB 20; Length 255;

Best Local Similarity 65.8%; Pred. No. 1.6e-50; Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

QY 1 MGRGVOLKRIENKINROVTFESRRSGLLKKAHEISVLCDAEVALVFFSSKGLPEFSTD 60  
 DB 1 MGRGVOLKRIENKINROVTFESRRSGLLKKAHEISVLCDAEVALVFFSSKGLPEFSTD 60  
 QY 61 SCMERILERYDRYLSKQVGVSDVNSWVLEHAKLKAARVELEKKNRPFGEEDLST 120  
 DB 61 SCMERILERYDRYLSKQVGVSDVNSWVLEHAKLKAARVELEKKNRPFGEEDLST 120  
 QY 121 SKELOSLEHODDAIKTSIRSRKNQAFESISALOKKDALODHNSLKKIKEREK-KT 179  
 DB 121 SKELOSLEHODDAIKTSIRSRKNQAFESISALOKKDALODHNSLKKIKEREK-KT 179  
 QY 180 GQOE--GOLVQCSNSSSVLLPQ 199  
 DB 181 AQOEQMDQOQNGHNPPLPQ 202

RESULT 13  
 AAW43109  
 ID AAW43109 standard; protein: 256 AA.  
 AC AAW43109;  
 XX 18-JUN-1998 (first entry)  
 DE APETALA1 gene product from Arabidopsis thaliana.  
 KW Transgenic plant; ectopically expressed; meristem gene: APETALA1;  
 KW API; CAULIFLOWER; CAL; LEAFY; LFY; reproductive development;  
 KW angiosperm.  
 OS Arabidopsis thaliana.  
 PN WO9746077-A1.  
 PD 11-DEC-1997.  
 PF 05-JUN-1996; 96WO-US09429.  
 PR 05-JUN-1996; 96WO-US09429.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Weigel D, Yanofsky MF;  
 DR WPI: 1998-041769/04.  
 DR N-PSDB; AAT86628.  
 PT Transgenic plant comprising an ectopically expressed floral meristem  
 PT gene - for promoting early reproductive development and controlling  
 PT the time of seed-derived crop harvest(s) in e.g. grapes, beans,  
 PT corn, wheat, etc  
 PS Claim 12; Page 120; 158pp; English.  
 CC This sequence represents a floral meristem identity gene product,  
 CC APETALA1 (API) from Arabidopsis thaliana. The invention relates to  
 CC a non-naturally occurring seed plant comprising a first ectopically  
 CC expressible nucleic acid encoding a first floral meristem identity gene  
 CC product, provided that the first nucleic acid is not ectopically  
 CC expressed due to a mutation in an endogenous TERMINAL FLOWER gene.  
 CC The invention describes a method of converting shoot meristem to floral  
 CC meristem, especially in order to promote early reproductive development,  
 CC in an angiosperm, which comprises introducing a first ectopically  
 CC expressible nucleic acid molecule encoding a first floral meristem  
 CC identity gene product into the angiosperm. Ectopic expression of the  
 CC floral meristem gene product in the shoot meristem tissue of the  
 CC transgenic plant, allows selection of the time of seed development in  
 CC the plant which can be useful for manipulating the time of crop harvest  
 CC in seed-derived crops such as grapes, beans, corn, wheat, rice, hop,

CC etc., or to hasten the breeding of e.g. tree species, for insect or  
 CC disease resistance.  
 XX SQ Sequence 256 AA;  
 Query Match 54.4%; Score 662.5; DB 19; Length 256;  
 Best Local Similarity 65.8%; Pred. No. 1.6e-50;  
 Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

QY 1 MGRGVOLKRIENKINROVTFESRRSGLLKKAHEISVLCDAEVALVFFSSKGLPEFSTD 60  
 DB 1 MGRGVOLKRIENKINROVTFESRRSGLLKKAHEISVLCDAEVALVFFSSKGLPEFSTD 60  
 QY 61 SCMERILERYDRYLSKQVGVSDVNSWVLEHAKLKAARVELEKKNRPFGEEDLST 120  
 DB 61 SCMERILERYDRYLSKQVGVSDVNSWVLEHAKLKAARVELEKKNRPFGEEDLST 120  
 QY 121 SKELOSLEHODDAIKTSIRSRKNQAFESISALOKKDALODHNSLKKIKEREK-KT 179  
 DB 121 SKELOSLEHODDAIKTSIRSRKNQAFESISALOKKDALODHNSLKKIKEREK-KT 179  
 QY 180 GQOE--GOLVQCSNSSSVLLPQ 199  
 DB 181 AQOEQMDQOQNGHNPPLPQ 202

RESULT 14  
 AAW39131  
 ID AAW39131 standard; protein: 256 AA.  
 AC AAW39131;  
 XX 08-JUN-1998 (first entry)  
 DE Arabidopsis floral meristem identity gene product. APETALA1.  
 KW Floral meristem identity gene product; APETALA1; API;  
 KW transgenic plant; angiosperm; seed development.  
 OS Arabidopsis thaliana.  
 PN WO9746078-A1.  
 PD 11-DEC-1997.  
 PF 05-JUN-1996; 96WO-US09453.  
 PR 05-JUN-1996; 96WO-US09453.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Yanofsky MF;  
 DR WPI: 1998-041770/04.  
 DR N-PSDB; AAV02760.  
 PT Nucleic acids encoding API floral meristem identity gene product  
 PT from cauliflower and maize - useful for promoting early reproductive  
 PT development and controlling the time of seed-derived crop harvest in  
 PT e.g. grapes, beans, corn, wheat, etc  
 PS Disclosure; Page 120-121; 156pp; English.  
 CC This protein comprises Arabidopsis thaliana floral meristem  
 CC identity gene product APETALA1 (API) that is involved in the  
 CC conversion of shoot meristem to floral meristem. Mutation of the  
 CC API gene (see AAV02760) results in replacement of basal flowers by  
 CC inflorescence shoots that are not subtended by flowers. The  
 CC invention relates to an expression vector comprising a nucleic  
 CC acid sequence encoding a floral meristem gene product operably  
 CC linked to a heterologous regulatory element (see AAV02770-75). The  
 CC floral meristem gene product is selected from API, LFY (LEAFY) and  
 CC CAL (CAULIFLOWER) (see AAW39131-38). The expression vector is used to

CC convert shoot meristem tissue to floral meristem tissue in  
CC transgenic plants, especially angiosperms or gymnosperms, thereby  
CC promoting early reproductive development in these plants. This can  
CC be used to manipulate the time of crop harvest and to hasten  
CC breeding time.

XX Sequence 256 AA;

Query Match 54.4%; Score 662.5; DB 19; Length 256;  
Best Local Similarity 65.8%; Pred. No. 1.6e-50;  
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

OY 1 MGRGVQLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
DB 1 MGRGVQLKRIENKINROVTFESKRRAGLLKKAHEISVLCDAEVALIVSSHKGLFEYSTD 60  
OY 61 SCMERILERYDRYLYSDKQVGRDVSQSENVYLEHAKEIKARVEYLEKNRNFMGEDLSTL 120  
DB 61 SCMERILERYERYSYAEKQVLAPESDVNTNMSMEYNRLKAKTELLERNQRYHVGEDLQAM 120  
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DB 121 SPEKLONLQEQDLTALKHIRTRKNQVLESTINELQKKERKALQEQNSMLSKQIKERERKILR 180  
OY 180 GQOE--GOLVCCSNSSSVLLPQ 199  
DB 181 AQOEQMDQONGHNMPPPLPQ 202

RESULT 15  
AAW43326

ID AAW43326 standard; Protein: 256 AA.

XX AAW43326;

XX 08-JUN-1998 (first entry)

DE Arabidopsis floral meristem identity gene product APETALA1.

KW Floral meristem identity gene: APETALA1; AP1; transgenic plant;  
KW angiosperm; seed development.

XX Arabidopsis thaliana.

XX W09746079-A1.

XX 11-DEC-1997.

XX 04-JUN-1997; 97WO-US09682.

XX 05-JUN-1996; 96US-0659188.

PA (REGC ) UNIV CALIFORNIA.

PI Yanofsky MF;

DR WPI: 1998-041771/04.

DR N-PSDB; AAV06018.

PT Use of floral meristem identity genes to convert shoot meristem to  
PT floral meristem - for promoting early reproductive development in  
PT the plants and control timing of seed-derived crop harvest(s) in  
PT e.g. grapes, beans, corn and wheat

XX Claim 6; Page 103-105; 147pp; English.

XX This protein comprises Arabidopsis thaliana floral meristem  
CC identity gene product APETALA1 (AP1) that is involved in the  
CC conversion of shoot meristem to floral meristem. Mutation of the  
CC AP1 gene (see AAV06018) results in replacement of basal flowers by  
CC inflorescence shoots that are not subtended by flowers. The  
CC invention relates to a recombinant nucleic acid molecule that  
CC comprises an inducible regulatory element (see AAV06025-28) operably

CC linked to a nucleic acid molecule (see AAV06018-24) encoding a floral  
CC meristem identity gene product (see AAW43326-33), especially AP1,  
CC CALIFLOWER (CAL) or LEAFY (LFY). The nucleic acids are used to  
CC convert shoot meristem tissue into floral meristem tissue in  
CC transgenic plants, thereby promoting early reproductive development  
CC in these plants. This can be useful for manipulating the time of  
CC crop harvest in seed-derived crops and to hasten breeding time.

XX Sequence 256 AA;

Query Match 54.4%; Score 662.5; DB 19; Length 256;  
Best Local Similarity 65.8%; Pred. No. 1.6e-50;  
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

OY 1 MGRGVQLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
DB 1 MGRGVQLKRIENKINROVTFESKRRAGLLKKAHEISVLCDAEVALIVSSHKGLFEYSTD 60  
OY 61 SCMERILERYDRYLYSDKQVGRDVSQSENVYLEHAKEIKARVEYLEKNRNFMGEDLSTL 120  
DB 61 SCMERILERYERYSYAEKQVLAPESDVNTNMSMEYNRLKAKTELLERNQRYHVGEDLQAM 120  
OY 121 SKELOSLSEHOLDAAIKSIRSRKNOAMFESTSALOKKDALODHNSLSLKIKERER-KT 179  
DB 121 SPEKLONLQEQDLTALKHIRTRKNQVLESTINELQKKERKALQEQNSMLSKQIKERERKILR 180  
OY 180 GQOE--GOLVCCSNSSSVLLPQ 199  
DB 181 AQOEQMDQONGHNMPPPLPQ 202

Search completed: January 27, 2003, 12:38:04  
Job time : 37 secs

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## OM protein - protein search, using sw model

Run on: January 27, 2003, 12:37:07 : Search time 15 seconds  
(without alignments)  
474.690 Million cell updates/sec

Title: US-09-981-087A-2

Perfect score: 1218

Sequence: 1 MGRGRVQLKRIENKINROVT.....LTPNSLLPAMLRPTTNE 242

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	662.5	54.4	255	2	US-08-576-156-2
5	662.5	54.4	256	3	US-08-659-188-2
6	662.5	54.4	256	3	US-08-655-227-2
7	662.5	54.4	256	3	US-08-655-241-2
8	662.5	54.4	256	4	US-09-398-326-2
9	662.5	54.4	300	2	US-08-592-214A-2
10	662.5	54.4	300	2	US-09-149-976-2
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33	621.5	51.0	251	3	US-09-149-976-12	Sequence 12, Appl
34	621.5	51.0	251	4	US-09-398-326-12	Sequence 12, Appl
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37	610.5	50.1	273	3	US-08-655-227-8	Sequence 8, Appl
38	610.5	50.1	273	3	US-08-655-241-8	Sequence 8, Appl
39	610.5	50.1	273	4	US-09-149-976-8	Sequence 8, Appl
40	610.5	50.1	273	4	US-09-398-326-8	Sequence 8, Appl
41	548	45.0	150	2	US-08-592-214A-14	Sequence 14, Appl
42	548	45.0	150	3	US-08-659-188-14	Sequence 14, Appl
43	548	45.0	150	3	US-08-655-227-14	Sequence 14, Appl
44	548	45.0	150	3	US-08-655-241-14	Sequence 14, Appl
45	548	45.0	150	3	US-09-149-976-14	Sequence 14, Appl

## ALIGNMENTS

RESULT 1  
US-09-067-800-2  
Sequence 2, Application US/09067800  
Patent No. 6198024  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
APPLICANT: Ferrandiz, Cristina  
TITLE OF INVENTION: Seed Plants Characterized by Delayed  
TITLE OF INVENTION: Seed Dispersal  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/067,800  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 2948  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 242 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-067-800-2  
Query Match 100.0%; Score 1218; DB 4; Length 242;  
Best Local Similarity 100.0%; Pred. No. 4 2e-107; Indels 0; Gaps 0;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 121 SKELOSLEHOLDAAIKSIRSRKNQAMFESISALOKKDKALODHNNSLKKIKEREKKTG 180
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Db 181 QOEGOLVOCSSSSVLLPOYCVTSSRDGFVERVGGENGASSLTEPNSLLPAMMLRPTTT 240
QY 241 NE 242
Db 241 NE 242
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## RESULT 2

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US-09-105-652-2
; Sequence 2, Application US/09105652
; Patent No. 6229068
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Marijnsen, Robert
; APPLICANT: Ferrandiz, Cristina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/105,652
; CURRENT FILING DATE: 1998-06-26
; EARLIER APPLICATION NUMBER: 60/051,030
; EARLIER FILING DATE: 1997-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRF
; ORGANISM: Arabidopsis sp.
US-09-105-652-2
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Query Match 100.0%; Score 1218; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 4.2e-107;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGRGVOLKRIENKINROYTFESKRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
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Db 121 SKELOSLEHOLDAAIKSIRSRKNQAMFESISALOKKDKALODHNNSLKKIKEREKKTG 180
QY 181 QOEGOLVOCSSSSVLLPOYCVTSSRDGFVERVGGENGASSLTEPNSLLPAMMLRPTTT 240
Db 181 QOEGOLVOCSSSSVLLPOYCVTSSRDGFVERVGGENGASSLTEPNSLLPAMMLRPTTT 240
QY 241 NE 242
Db 241 NE 242
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## RESULT 3

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US-09-349-677-2
; Sequence 2, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
```

```
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-349-677-2
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Query Match 100.0%; Score 1218; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 4.2e-107;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MGRGVOLKRIENKINROYTFESKRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
Db 1 MGRGVOLKRIENKINROYTFESKRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
QY 61 SCMERILERDRYLSDKQVGRDVSQSENWVLEHAHLKARVELEKNRNFMGEDLDSTL 120
Db 61 SCMERILERDRYLSDKQVGRDVSQSENWVLEHAHLKARVELEKNRNFMGEDLDSTL 120
QY 121 SKELOSLEHOLDAAIKSIRSRKNQAMFESISALOKKDKALODHNNSLKKIKEREKKTG 180
Db 121 SKELOSLEHOLDAAIKSIRSRKNQAMFESISALOKKDKALODHNNSLKKIKEREKKTG 180
QY 181 QOEGOLVOCSSSSVLLPOYCVTSSRDGFVERVGGENGASSLTEPNSLLPAMMLRPTTT 240
Db 181 QOEGOLVOCSSSSVLLPOYCVTSSRDGFVERVGGENGASSLTEPNSLLPAMMLRPTTT 240
QY 241 NE 242
Db 241 NE 242
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## RESULT 4

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US-08-576-156-2
; Sequence 2, Application US/08576156
; Patent No. 5844119
; GENERAL INFORMATION:
; APPLICANT: Weigel, Detlef
; TITLE OF INVENTION: Genetically Modified Plants Having Modulated
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
```

Query Match	54.4%	Score 662.5	DB 2	Length 255
Best Local Similarity	65.8%	Pred. No. 9.6e-55		
Matches 133	Conservative 33	Mismatches 33	Indels 3	Gaps 2

RESULT 5  
US-08-659-188-2  
; Sequence 2, Application US/08659188  
; Patent No. 6002069

APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early  
TITLE OF INVENTION: Reproductive Development and Methods of Making Same  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
City: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

Query Match	54.4%	Score 662.5	DB 3	Length 256
Best Local Similarity	65.8%	Pred. No. 9.7e-55		
Matches 133	Conservative 33	Mismatches 33	Indels 3	Gaps 2

RESULT 6  
US-08-655-227-2

APPLICANT: Yanofsky, Martin F.  
 TITLE OF INVENTION: Maize and Cauliflower APEPAL1 Gene  
 TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 City: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/655,227  
 FILING DATE: 05-JUN-1996  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-UD 2143  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:

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; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-655-227-2

Query Match          54.4%; Score 662.5; DB 3; Length 256;
Best Local Similarity 65.8%; Pred. No. 9.7e-55;
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

OY 1 MGRGVOLKRIENKINROVTFSKRRSGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
    |||||||
Db 1 MGRGVOLKRIENKINROVTFSKRRAGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
    |||||||

OY 61 SCMERILERYDRYLSKQLVGRDVOSQSENNVLEHAHAKARVELEKKNRMFGEDLSL 120
    |||||
Db 61 SCMERILERYDRYLSKQLVGRDVOSQSENNVLEHAHAKARVELEKKNRMFGEDLSL 120
    |||||

OY 121 SKEIQLSEHQLDAIKSIRSRKNQAMFESISALQKKDALQDHNNSLLKIKERK-KT 179
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Db 121 SPEIQLNEQLDTALKHIFTRKNQMLMESINELQKKERAIQDQNSMLSKQIKEREKILR 180
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OY 180 GQOE--GQLVQCSNSSSVLLPQ 199
    |||
Db 181 AOOEQWDOQNOGHNMPPPLPQ 202
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RESULT 7
US-08-655-241-2
; Sequence 2, Application US/08655241
; Patent No. 6025543
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
; TITLE OF INVENTION: Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; ADDRESSSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,241
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: CLASS 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-655-241-2

Query Match          54.4%; Score 662.5; DB 3; Length 256;
Best Local Similarity 65.8%; Pred. No. 9.7e-55;
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

OY 1 MGRGVOLKRIENKINROVTFSKRRSGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
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Db 1 MGRGVOLKRIENKINROVTFSKRRAGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
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OY 61 SCMERILERYDRYLSKQLVGRDVOSQSENNVLEHAHAKARVELEKKNRMFGEDLSL 120
|||||
Db 61 SCMERILERYDRYLSKQLVGRDVOSQSENNVLEHAHAKARVELEKKNRMFGEDLSL 120
|||||

OY 121 SKEIQLSEHQLDAIKSIRSRKNQAMFESISALQKKDALQDHNNSLLKIKERK-KT 179
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Db 121 SPEIQLNEQLDTALKHIFTRKNQMLMESINELQKKERAIQDQNSMLSKQIKEREKILR 180
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OY 180 GQOE--GQLVQCSNSSSVLLPQ 199
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Db 181 AOOEQWDOQNOGHNMPPPLPQ 202
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RESULT 8
US-09-398-326-2
; Sequence 2, Application US/09398326
; Patent No. 635863
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; ADDRESSSEE: Campbell and Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,326
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/659,188
; FILING DATE: 05-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-398-326-2

Query Match          54.4%; Score 662.5; DB 4; Length 256;
Best Local Similarity 65.8%; Pred. No. 9.7e-55;
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

OY 1 MGRGVOLKRIENKINROVTFSKRRSGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
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Db 1 MGRGVOLKRIENKINROVTFSKRRAGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
    |||||||

OY 61 SCMERILERYDRYLSKQLVGRDVOSQSENNVLEHAHAKARVELEKKNRMFGEDLSL 120
    |||||
Db 61 SCMERILERYDRYLSKQLVGRDVOSQSENNVLEHAHAKARVELEKKNRMFGEDLSL 120
    |||||

OY 121 SKEIQLSEHQLDAIKSIRSRKNQAMFESISALQKKDALQDHNNSLLKIKERK-KT 179
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Db 121 SPEIQLNEQLDTALKHIFTRKNQMLMESINELQKKERAIQDQNSMLSKQIKEREKILR 179
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Db 121 SPEKLONEQOQDLTKHTRKNOIWESEINELQKKEKAIQEOINSMLSKQIKEREKILR 180  
QY 180 GOOE--GOLVOCSSSSVLLPQ 199  
Db 181 AOOEQWDOQNOGHNMPPPLPQ 202

## RESULT 9

US-08-592-214A-2  
; Sequence 2, Application US/08592214A  
; Patent No. 5811536  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
; TITLE OF INVENTION: Genes and Methods of Using Same  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,214A  
; FILING DATE: 26-JAN-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1927  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 300 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-592-214A-2

Query Match 54.4%; Score 662.5; DB 2; Length 300;  
Best Local Similarity 65.8%; Pred. No. 1.2e-54;  
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

QY 1 MGRGVOLKRIENKINROVTFESKRRSGGLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINROVTFESKRRSGGLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
QY 61 SCMERILERYRYLYSDKOLVGRDVSQSENVYLEHAKLKARVEVLEKKNRNPGEIDLSTL 120  
Db 61 SCMERILERYRYLYSDKOLVGRDVSQSENVYLEHAKLKARVEVLEKKNRNPGEIDLSTL 120  
QY 121 SKELOSLEHOLAIAIKSIRSKNOAMFESISALOKKDALODHNNSLKTIKEREK-KT 179  
Db 121 SPEKLONEQOQDLTKHTRKNOIWESEINELQKKEKAIQEOINSMLSKQIKEREKILR 180  
QY 180 GOOE--GOLVOCSSSSVLLPQ 199  
Db 181 AOOEQWDOQNOGHNMPPPLPQ 202

RESULT 10  
US-09-149-976-2  
; Sequence 2, Application US/09149976  
; Patent No. 6127123  
; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.  
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
; TITLE OF INVENTION: Genes and Methods of Using Same  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/149,976  
; FILING DATE: 09-SEP-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/592,214  
; FILING DATE: 26-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 3291  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 300 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-149-976-2

Query Match 54.4%; Score 662.5; DB 3; Length 300;  
Best Local Similarity 65.8%; Pred. No. 1.2e-54;  
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

QY 1 MGRGVOLKRIENKINROVTFESKRRSGGLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINROVTFESKRRSGGLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
QY 61 SCMERILERYRYLYSDKOLVGRDVSQSENVYLEHAKLKARVEVLEKKNRNPGEIDLSTL 120  
Db 61 SCMERILERYRYLYSDKOLVGRDVSQSENVYLEHAKLKARVEVLEKKNRNPGEIDLSTL 120  
QY 121 SKELOSLEHOLAIAIKSIRSKNOAMFESISALOKKDALODHNNSLKTIKEREK-KT 179  
Db 121 SPEKLONEQOQDLTKHTRKNOIWESEINELQKKEKAIQEOINSMLSKQIKEREKILR 180  
QY 180 GOOE--GOLVOCSSSSVLLPQ 199  
Db 181 AOOEQWDOQNOGHNMPPPLPQ 202

RESULT 11  
US-08-592-214A-4  
; Sequence 4, Application US/08592214A  
; Patent No. 5811536  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
; TITLE OF INVENTION: Genes and Methods of Using Same  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California

COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,214A  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1927  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-592-214A-4

Query Match 53.7%; Score 654; DB 2; Length 253;  
Best Local Similarity 66.5%; Pred. No. 6e-54;  
Matches 123; Conservative 36; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGRGVOLKRIENKINQVTFKRSGLKKAHEISVLCDAEVALVFSKGLFEYSTD 60  
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DB 1 MGRGVOLKRIENKINQVTFKRSGLKKAHEISVLCDAEVALVFSKGLFEYSTD 60  
|||||  
QY 61 SCMERILEYDRYLSKQVGRDVSQSENWVLEHAKLKARVELEKKNPMGEDLSL 120  
|||||  
DB 61 SCMERILEYDRYLSKQVGRDVSQSENWVLEHAKLKARVELEKKNPMGEDLSL 120  
|||||  
QY 121 SKLEQSLHOLDAAIKRSRKNQAMFESISALOKKDALODHNNLSLKIKEREKKTG 180  
|||||  
DB 121 SKLEQSLHOLDAAIKRSRKNQAMFESISALOKKDALODHNNLSLKIKEREKKTG 180  
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QY 181 QOEGQ 185  
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DB 181 AQOEG 185

RESULT 12  
US-08-659-188-4  
Sequence 4, Application US/08659188  
Patent No. 6002069  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Seed plants exhibiting inducible Early  
NUMBER OF SEQUENCES: 26  
REPRODUCTIVE Development and Methods of Making Same  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/659,188  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1946  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-659-188-4

Query Match 53.7%; Score 654; DB 3; Length 253;  
Best Local Similarity 66.5%; Pred. No. 6e-54;  
Matches 123; Conservative 36; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGRGVOLKRIENKINQVTFKRSGLKKAHEISVLCDAEVALVFSKGLFEYSTD 60  
|||||  
DB 1 MGRGVOLKRIENKINQVTFKRSGLKKAHEISVLCDAEVALVFSKGLFEYSTD 60  
|||||  
QY 61 SCMERILEYDRYLSKQVGRDVSQSENWVLEHAKLKARVELEKKNPMGEDLSL 120  
|||||  
DB 61 SCMERILEYDRYLSKQVGRDVSQSENWVLEHAKLKARVELEKKNPMGEDLSL 120  
|||||  
QY 121 SKLEQSLHOLDAAIKRSRKNQAMFESISALOKKDALODHNNLSLKIKEREKKTG 180  
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DB 121 SKLEQSLHOLDAAIKRSRKNQAMFESISALOKKDALODHNNLSLKIKEREKKTG 180  
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QY 181 QOEGQ 185  
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DB 181 AQOEG 185

RESULT 13  
US-08-655-227-4  
Sequence 4, Application US/08655227  
Patent No. 6025483  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Maize and Cauliflower APTETAL Gene  
NUMBER OF SEQUENCES: 26  
PRODUCTS AND Nucleic Acid Molecules Encoding Same  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/655,227  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 2143  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein



Mon Feb 3 09:47:24 2003

us-09-981-087a-2.ra1

Page 8

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Job time : 16 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:39:07 ; Search time 11 seconds  
(without alignments)  
443.928 Million cell updates/sec

Title: US-09-981-087a-2  
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Sequence: 1 MGRGVOLKRIENKINROVT.....LTEDNSLLPAMMLRPTTNE 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database :

Published.Applications\_AA:\*  
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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1218	100.0	242	9	US-09-978-729A-2
2	1218	100.0	242	9	US-09-981-087A-2
3	1218	100.0	242	9	US-09-978-382A-2
4	1218	100.0	242	9	US-09-978-740A-2
5	1218	100.0	242	10	US-09-978-730-2
6	662.5	54.4	256	9	US-09-853-450-2
7	654	53.7	253	9	US-09-853-450-4
8	647	53.1	255	9	US-09-853-450-6
9	627	51.5	255	9	US-09-853-450-10
10	621.5	50.1	251	9	US-09-853-450-12
11	610.5	50.1	273	9	US-09-853-450-8
12	548	45.0	150	9	US-09-853-450-14
13	484.5	39.8	248	9	US-09-853-450-28
14	463.5	38.1	250	9	US-09-853-450-30
15	443	36.4	237	9	US-09-853-450-32
16	396.5	32.6	214	9	US-09-853-450-34
17	390.5	32.1	240	10	US-09-970-624-2
18	381	31.3	248	9	US-09-978-729A-4
19	381	31.3	248	9	US-09-981-087A-4

20	381	31.3	248	9	US-09-978-382A-4	Sequence 4, Appli
21	381	31.3	248	9	US-09-978-740A-4	Sequence 4, Appli
22	381	31.3	248	10	US-09-978-730-4	Sequence 4, Appli
23	378	31.0	246	9	US-09-978-729A-6	Sequence 6, Appli
24	378	31.0	246	9	US-09-981-087A-6	Sequence 6, Appli
25	378	31.0	246	9	US-09-978-382A-6	Sequence 6, Appli
26	378	31.0	246	9	US-09-978-740A-6	Sequence 6, Appli
27	378	31.0	246	10	US-09-978-730-6	Sequence 6, Appli
28	328	26.9	220	9	US-09-853-450-38	Sequence 38, Appli
29	314.5	25.8	210	9	US-09-853-450-36	Sequence 36, Appli
30	310	25.5	173	9	US-09-853-450-40	Sequence 40, Appli
31	285.5	23.4	192	9	US-09-853-450-50	Sequence 50, Appli
32	242	19.9	105	10	US-09-767-215-10	Sequence 10, Appli
33	225	18.5	521	10	US-09-749-728B-19	Sequence 19, Appli
34	221	18.1	365	10	US-09-876-187-4	Sequence 4, Appli
35	221	18.1	365	10	US-09-749-728B-15	Sequence 15, Appli
36	218.5	17.9	507	10	US-09-876-187-2	Sequence 2, Appli
37	218.5	17.9	507	10	US-09-749-728B-13	Sequence 13, Appli
38	215.5	17.7	465	10	US-09-749-728B-17	Sequence 17, Appli
39	215.5	17.7	473	10	US-09-876-187-6	Sequence 6, Appli
40	215.5	17.7	473	10	US-09-876-187-8	Sequence 8, Appli
41	182.5	15.0	676	10	US-09-801-368-302	Sequence 302, App
42	170.5	14.0	452	10	US-09-801-368-336	Sequence 336, App
43	150	12.3	286	10	US-09-801-368-188	Sequence 188, App
44	113	9.3	689	9	US-10-108-605-305	Sequence 305, App
45	112	9.2	2568	10	US-09-866-108-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
US-09-978-729A-2  
Sequence 2, Application US/09978729A

Patent No. US20020178465A1  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
APPLICANT: Lilljegen, Sarah  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
FILE REFERENCE: 19452A-000950US  
CURRENT APPLICATION NUMBER: US/09/978, 729A  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: US 60/090, 649  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: US 09/339, 998  
PRIOR FILING DATE: 1999-06-25  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 242  
TYPE: PRT  
ORGANISM: Arabidopsis sp.

US-09-978-729A-2

Query Match 100.0%; Score 1218; DB 9; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.8e-92;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGVOLKRIENKINROVTFSSRRSGGLKKAHETSVCDAEVALIVFSSKGLPEYSTD 60  
DB 1 MGRGVOLKRIENKINROVTFSSRRSGGLKKAHETSVCDAEVALIVFSSKGLPEYSTD 60  
QY 61 SCMERILRYDRYLXSDKOLVGRDVSQSENNVLEHAHLKARVEYLEKRRNFMGEDDLSL 120  
DB 61 SCMERILRYDRYLXSDKOLVGRDVSQSENNVLEHAHLKARVEYLEKRRNFMGEDDLSL 120  
QY 121 SLKEIQLSEHOLDAAIKIRSRKKNOAMFESISALOKKKAALODHNNLSLKKIKEREKKTG 180  
DB 121 SLKEIQLSEHOLDAAIKIRSRKKNOAMFESISALOKKKAALODHNNLSLKKIKEREKKTG 180  
QY 181 OQEGOLVGCSSNSSSVLLPQYCVTSRRDGFVERVGGENGCGASSLTPEPNSLLPAMMLRPTTT 240

Db 181 QOEGOLVOCSSSVLLPQYCVTSSRDGFVERVGGENGASSLTPNSLLPAMMLRPTTT 240  
QY 241 NE 242  
Db 241 NE 242

## RESULT 2

US-09-981-087a-2  
; Sequence 2, Application US/09981087A  
; Patent No. US20020178466A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegren, Sarah  
; APPLICANT: Farrandiz, Cristina  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-0009400S  
; CURRENT APPLICATION NUMBER: US/09/981,087A  
; CURRENT FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-981-087a-2

Query Match 100.0%; Score 1218; DB 9; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1,8e-92;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
QY 61 SCMERILERYDRLYSDKOLVGRDVSQSENNVLEHAKKLARVEVLEKKNRNFMEGDLDSL 120  
Db 61 SCMERILERYDRLYSDKOLVGRDVSQSENNVLEHAKKLARVEVLEKKNRNFMEGDLDSL 120  
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Db 181 QOEGOLVOCSSSVLLPQYCVTSSRDGFVERVGGENGASSLTPNSLLPAMMLRPTTT 240  
QY 241 NE 242  
Db 241 NE 242

## RESULT 3

US-09-978-382a-2  
; Sequence 2, Application US/09978382A  
; Publication No. US20020194647A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegren, Sarah  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-0009300S  
; CURRENT APPLICATION NUMBER: US/09/978,382A  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/090,649

; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-978-382a-2

Query Match 100.0%; Score 1218; DB 9; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1,8e-92;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
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Db 61 SCMERILERYDRLYSDKOLVGRDVSQSENNVLEHAKKLARVEVLEKKNRNFMEGDLDSL 120  
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Db 121 SKEIQLSLEHOLDALIKSIRSRKNQAMFESISALOKKDALODHNNSLKKIKEREKKTG 180  
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Db 181 QOEGOLVOCSSSVLLPQYCVTSSRDGFVERVGGENGASSLTPNSLLPAMMLRPTTT 240  
QY 241 NE 242  
Db 241 NE 242

## RESULT 4

US-09-978-740a-2  
; Sequence 2, Application US/09978740A  
; Publication No. US20030005481A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegren, Sarah  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-0009600S  
; CURRENT APPLICATION NUMBER: US/09/978,740A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/090,649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339,998  
; PRIOR FILING DATE: 1999-06-25  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-978-740a-2

Query Match 100.0%; Score 1218; DB 9; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1,8e-92;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
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Db 61 SCMERILERYDRLYSDKOLVGRDVSQSENNVLEHAKKLARVEVLEKKNRNFMEGDLDSL 120

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Db 241 NE 242

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RESULT 5
US-09-978-730-2
; Sequence 2, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljeqren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Plasmid Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-0009200S
; CURRENT APPLICATION NUMBER: US/09/978, 730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090, 649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339, 998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-730-2

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Query Match          100.0%; Score 1218; DB 10; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.8e-92;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGRGVQLRIENKINRQVTSKRSGGLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
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Db 61 SCMERILERYDRYLYSDKQVGRDVSQSENNVLEHAKLKAHEVLEKKNRPMGEDDLSL 120
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    |||
Db 121 SKEIQLSLEHQLDAIKIRSRRKNQAMFESISALOKKDALODHNNLSLKIKEREKKTG 180
OY 181 QOEGOLVOCSSSSSVLLPQYCVTSRRDGFVERVGGENGASSLTPNSLLPAMMLRPTTT 240
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Db 181 QOEGOLVOCSSSSSVLLPQYCVTSRRDGFVERVGGENGASSLTPNSLLPAMMLRPTTT 240
OY 241 NE 242
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Db 241 NE 242

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RESULT 6
US-09-853-450-2
; Sequence 2, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants

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; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853, 450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: APETALAI (AP1)
US-09-853-450-2

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Query Match          54.4%; Score 662.5; DB 9; Length 256;
Best Local Similarity 65.8%; Pred. No. 4.1e-47;
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

OY 1 MGRGVQLRIENKINRQVTSKRSGGLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
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Db 1 MGRGVQLRIENKINRQVTSKRSGGLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
OY 61 SCMERILERYDRYLYSDKQVGRDVSQSENNVLEHAKLKAHEVLEKKNRPMGEDDLSL 120
    |||
Db 61 SCMERILERYDRYLYSDKQVGRDVSQSENNVLEHAKLKAHEVLEKKNRPMGEDDLSL 120
OY 121 SKEIQLSLEHQLDAIKIRSRRKNQAMFESISALOKKDALODHNNLSLKIKEREKKT 179
    |||
Db 121 SKEIQLSLEHQLDAIKIRSRRKNQAMFESISALOKKDALODHNNLSLKIKEREKKT 180
OY 180 GQOE--GOLVOCSSSSSVLLPQ 199
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Db 181 AQEQWQDQNGHNPPLPQ 202

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RESULT 7
US-09-853-450-4
; Sequence 4, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853, 450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Brassica oleracea
; FEATURE:
; OTHER INFORMATION: APETALAI (AP1)
US-09-853-450-4

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Query Match          53.7%; Score 654; DB 9; Length 253;
Best Local Similarity 66.5%; Pred. No. 2e-46;
Matches 123; Conservative 36; Mismatches 26; Indels 0; Gaps 0;

OY 1 MGRGVQLRIENKINRQVTSKRSGGLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
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Db 1 MGRGVQLRIENKINRQVTSKRSGGLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
OY 61 SCMERILERYDRYLYSDKQVGRDVSQSENNVLEHAKLKAHEVLEKKNRPMGEDDLSL 120
    |||
Db 61 SCMERILERYDRYLYSDKQVGRDVSQSENNVLEHAKLKAHEVLEKKNRPMGEDDLSL 120
OY 121 SKEIQLSLEHQLDAIKIRSRRKNQAMFESISALOKKDALODHNNLSLKIKEREKKTG 180
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Db 121 SKEIQLSLEHQLDAIKIRSRRKNQAMFESISALOKKDALODHNNLSLKIKEREKKTG 180

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Db 121 SPKEQLNLEQOQDITALKHRSRKNQMLMTDSINELQREKAIQEOQNSMLSKQIKERENVLR 180  
 QY 181 OQEQ 185  
 Db 181 AQOQ 185

## RESULT 8

US-09-853-450-6  
 ; Sequence 6, Application US/09853450  
 ; Publication No. US20020194645A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yanoofsky, Martin F.  
 ; APPLICANT: Pelaz, Soraya  
 ; APPLICANT: Ditta, Gary  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants  
 ; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development  
 ; FILE REFERENCE: 19452A-002400US  
 ; CURRENT APPLICATION NUMBER: US/09/853,450  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 255  
 ; TYPE: PRT  
 ; ORGANISM: Brassica oleracea var. botrytis  
 ; FEATURE:  
 ; OTHER INFORMATION: APETALAI (AP1)  
 US-09-853-450-6

Query Match 53.1%; Score 647; DB 9; Length 255;  
 Best Local Similarity 65.9%; Pred. No. 7.6e-46;  
 Matches 122; Conservative 35; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGRGVOLKRIENKINROVTFPSRRSGLLKKAHEISVLCDAEVALIVPSSGKLFPEYSTD 60  
 Db 1 MGRGVOLKRIENKINROVTFPSRRSGLLKKAHEISVLCDAEVALIVPSSGKLFPEYSTD 60  
 QY 61 SCMERILERYDRYLYSDKQVGRDVSQSENVYLEHAKLKARVEVLEKRNKRNMGEDLD 120  
 Db 61 SCMERILERYDRYLYSDKQVGRDVSQSENVYLEHAKLKARVEVLEKRNKRNMGEDLD 120  
 QY 121 SLKELQSLLEHOLDAAIKSIRSRKNQAMFESISALOKKDALODHNSLLKTIKEREKK 180  
 Db 121 SPKEQLNLEQOQDITALKHRSRKNQMLMTDSINELQREKAIQEOQNSMLSKQIKERENVLR 180  
 QY 181 OQEQ 185  
 Db 181 AQOQ 185

## RESULT 9

US-09-853-450-10  
 ; Sequence 10, Application US/09853450  
 ; Publication No. US20020194645A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yanoofsky, Martin F.  
 ; APPLICANT: Pelaz, Soraya  
 ; APPLICANT: Ditta, Gary  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants  
 ; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development  
 ; FILE REFERENCE: 19452A-002400US  
 ; CURRENT APPLICATION NUMBER: US/09/853,450  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 10  
 ; LENGTH: 255  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:

; OTHER INFORMATION: CAULIFLOWER (CAL)  
 US-09-853-450-10

Query Match 51.5%; Score 627; DB 9; Length 255;  
 Best Local Similarity 53.6%; Pred. No. 3.2e-44;  
 Matches 128; Conservative 47; Mismatches 54; Indels 10; Gaps 3;

QY 1 MGRGVOLKRIENKINROVTFPSRRSGLLKKAHEISVLCDAEVALIVPSSGKLFPEYSTD 60  
 Db 1 MGRGVOLKRIENKINROVTFPSRRSGLLKKAHEISVLCDAEVALIVPSSGKLFPEYSTD 60  
 QY 61 SCMERILERYDRYLYSDKQVGRD--VSQSENVYLEHAKLKARVEVLEKRNKRNMGEDLD 118  
 Db 61 SCMERILERYDRYLYSDKQVGRD--VSQSENVYLEHAKLKARVEVLEKRNKRNMGEDLD 120  
 QY 119 SLKELQSLLEHOLDAAIKSIRSRKNQAMFESISALOKKDALODHNSLLKTIKEREKK 178  
 Db 121 PMSKDLQNLLEQOQLELALHRSRKNQMLMTDSINELQREKAIQEOQNSMLSKQIKERENVLR 180  
 QY 179 TGOQEGOLVQCSNS--SSVLLPQ-----YCVTSRDEGFEVERVGEENGAGASLTPEPNSL 229  
 Db 181 LKTKQTCQEQLRNSVDVDPQPPFQHPHLYMIAHQTSFPLNNGGLYQGEDQTARRRNNL 239

## RESULT 10

US-09-853-450-12  
 ; Sequence 12, Application US/09853450  
 ; Publication No. US20020194645A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yanoofsky, Martin F.  
 ; APPLICANT: Pelaz, Soraya  
 ; APPLICANT: Ditta, Gary  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants  
 ; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development  
 ; FILE REFERENCE: 19452A-002400US  
 ; CURRENT APPLICATION NUMBER: US/09/853,450  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 251  
 ; TYPE: PRT  
 ; ORGANISM: Brassica oleracea  
 ; FEATURE:  
 ; OTHER INFORMATION: CAULIFLOWER (CAL)  
 US-09-853-450-12

Query Match 51.0%; Score 621.5; DB 9; Length 251;  
 Best Local Similarity 60.2%; Pred. No. 9e-44;  
 Matches 121; Conservative 42; Mismatches 35; Indels 3; Gaps 2;

QY 1 MGRGVOLKRIENKINROVTFPSRRSGLLKKAHEISVLCDAEVALIVPSSGKLFPEYSTD 60  
 Db 1 MGRGVOLKRIENKINROVTFPSRRSGLLKKAHEISVLCDAEVALIVPSSGKLFPEYSTD 60  
 QY 61 SCMERILERYDRYLYSDKQVGRD--VSQSENVYLEHAKLKARVEVLEKRNKRNMGEDLD 118  
 Db 61 SCMERILERYDRYLYSDKQVGRD--VSQSENVYLEHAKLKARVEVLEKRNKRNMGEDLD 120  
 QY 119 SLKELQSLLEHOLDAAIKSIRSRKNQAMFESISALOKKDALODHNSLLKTIKEREKK 178  
 Db 121 SISKELQSLLEHOLDAAIKSIRSRKNQAMFESISALOKKDALODHNSLLKTIKEREKK 180  
 QY 179 TGOQEGOLVQCSNS--SSVLLPQ 199  
 Db 181 LKTKQTCQEQLRNSVDVDPQPPFQHPHLYMIAHQTSFPLNNGGLYQGEDQTARRRNNL 239

## RESULT 11

US-09-853-450-8  
 ; Sequence 8, Application US/09853450  
 ; Publication No. US20020194645A1

```

; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: APELAL1 (AP1)
US-09-853-450-8
```

```

Query Match          50.1%; Score 610.5; DB 9; Length 273;
Best Local Similarity 49.1%; Pred. No. 7.9e-43;
Matches 133; Conservative 40; Mismatches 59; Indels 39; Gaps 4;
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```

OY 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVFSSKGLPEYSTD 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVFSPKGLPEYATD 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 SCMERILERDYRYLSDKQVGRDVSQSENNVLEHAKLKARVEVLEKKNRNFGEIDL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SMDKILERYERYSAEKALISAESSESGNMCHERYRLKAKETIÖKCHKHLMGDELSL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 121 SKEIÖSLEHÖDAIKSIRSKKNQAFESISALOKKDAKALDHNNSLTIKKEKKTG 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 NKEIÖQÖEQÖDSSILKHSRSHLMAESISELÖKERSIÖENKALÖKELAEÖKAVA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 181 ---QÖEGÖLVÖCSNSSSVLLPÖYCVTSSRDGFVERV-----GGE 216
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 SMOÖQÖQÖQVQMDQÖTHA---QAOISSSSSSSSSMÖROÖQÖGLPPHNICPPILTMGDRGE 237
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 217 NGGASSLTPENSL-----LPAWML 235
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 LAAAAAÖÖQÖPLPGÖAQÖPÖLRIAGLPPWML 268
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```

RESULT 12
US-09-853-450-14
; Sequence 14, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Brassica oleracea var. botrytis
; FEATURE:
; OTHER INFORMATION: CAULIFLOWER (CAL)
US-09-853-450-14
```

```

Query Match          45.0%; Score 548; DB 9; Length 150;
Best Local Similarity 68.5%; Pred. No. 4.7e-38;
Matches 102; Conservative 31; Mismatches 14; Indels 2; Gaps 1;
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```

OY 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVFSSKGLPEYSTD 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVFSSKGLPEYSTD 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 SCMERILERDYRYLSDKQVGRD--VSQSENNVLEHAKLKARVEVLEKKNRNFGEIDL 118
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SCMEKVLERYERYSAEQÖLKPDPSHVNAQÖTMSMEYSRLAKIKELMRNÖRHYGDELE 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 119 SLSKEIÖSLEHÖDAIKSIRSKKNQAM 147
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SISKEIÖNLEQÖLDTSSKHSRKNQML 149
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```

RESULT 13
US-09-853-450-28
; Sequence 28, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 28
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: SEPALLAT1 (SEP1)
US-09-853-450-28
```

```

Query Match          39.8%; Score 484.5; DB 9; Length 248;
Best Local Similarity 44.0%; Pred. No. 1.3e-32;
Matches 109; Conservative 46; Mismatches 80; Indels 13; Gaps 4;
```

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OY 1 MGRGVOLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIVFSSKGLPEYSTD 60
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Db 1 MGRGVOLKRIENKINROVTFEPKRRNGLLKKAHEISVLCDAEVALIVFSSKGLPEYSTD 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 SCMERILERDYRYLSDKQVGRDVSQSENNVLEHAKLKARVEVLEKKNRNFGEIDL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SMLKTLDRYÖKCSYGSIEVNNKPAKELENSRYEYLKLGREYENLÖROÖRNLLGDLGPL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 121 SKEIÖSLEHÖDAIKSIRSKKNQAFESISALOKKDAKALDHNNSLTIKKEKKTG 176
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 NKEIÖQÖEQÖDSSILKHSRSHLMAESISELÖKERSIÖENKALÖKELAEÖKAVA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 177 KKTGOÖEG--ÖLVÖCSN---SSSVLLPÖYCVTSSRDGFVERVGGENQASSLTPEN--N 227
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 HHMGWEGEGEÖNVTYAHHÖAQÖSGLYÖPLECNPTLÖMGIDNPFVCSÖITATTIÖAQÖPEN 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 228 SLTPAWML 235
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 GYIPGWMML 248
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```

RESULT 14
US-09-853-450-30
; Sequence 30, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
```



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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:34:12 ; Search time 11 Seconds

912.479 million cell updates/sec

Title: US-09-981-087A-2

Perfect score: 1218  
Sequence: 1 MGRGRVQLKRIENKINQVT.....LTPENSLLPAMMLRPTTNE 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1218	100.0	242	1	AGLE_ARATH	Q38876 arabidopsis
2	1112.5	91.3	241	1	AGLE_SINAL	Q41274 sinapis
3	743	61.0	250	1	AGLE_SOUTO	Q42429 solanum tub
4	731	60.0	250	1	AGLE_SOLCO	Q22378 solanum tub
5	709.5	58.3	227	1	AGLE_LYCES	Q40170 lycopersicc
6	662.5	54.4	256	1	AP1_ARATH	P35631 arabidopsis
7	656	53.9	254	1	AP1_SINAL	Q41276 sinapis alba
8	509	41.8	233	1	CMB1-DINCA	Q39685 dianthus ce
9	484.5	39.8	248	1	AGLE_ARATH	P29382 arabidopsis
10	472	38.8	241	1	AGLE_PETHY	Q00349 petunia hy
11	463.5	38.1	250	1	AGLE_ARATH	P29384 arabidopsis
12	461	37.8	251	1	AGLE_ARATH	Q2246 arabidopsis
13	449.5	36.9	254	1	AGLE_SINAL	Q04057 sinapis alba
14	449	36.9	224	1	AGLE_LYCES	Q42484 lycopersicc
15	446	36.6	250	1	AGLE_ARADE	Q38694 aranda debc
16	442	36.3	252	1	AGLE_ARATH	P29386 arabidopsis
17	432.5	35.5	258	1	AGLE_ARATH	P29383 arabidopsis
18	427	35.1	244	1	AG13_ARATH	Q38837 arabidopsis
19	416.5	34.2	248	1	AG_TOBAC	Q43585 nicotiana gl
20	415	34.1	242	1	AG_PETHY	Q40872 panax gins
21	412	33.8	242	1	AG_PETHY	Q40885 petunia hy
22	403	33.1	230	1	AG11_ARATH	Q38836 arabidopsis
23	403	33.1	252	1	AG_BRANA	Q01540 brassica na
24	401.5	33.0	248	1	AG_LYCES	Q40168 lycopersicc
25	399	32.8	252	1	AG_ARATH	P17899 arabidopsis
26	396.5	32.6	214	1	SOC1_ARATH	Q64645 arabidopsis
27	381	31.0	246	1	AGL1_ARATH	P29381 arabidopsis
28	378	31.0	246	1	AGL5_ARATH	P29385 arabidopsis
29	376.5	30.9	221	1	AGL1_ARATH	Q38838 arabidopsis
30	373.5	30.7	228	1	AG14_ARATH	Q38216 arabidopsis
31	356	29.2	219	1	AG19_ARATH	Q82743 arabidopsis
32	354.5	29.1	264	1	AG15_BRANA	Q39285 brassica na
33	344.5	28.3	265	1	JOIN_LYCES	Q91uv6 lycopersicc

34	344	28.2	26.8	1	AG15_ARATH	Q3884f1	arabidopsiss1
35	332.5	27.3	21.1	1	AG12_ARATH	Q3884f1	arabidopsiss1
36	325.5	26.7	24.0	1	SVP_ARATH	09f9c1	arabidopsiss1
37	325	26.7	232	1	AP3_ARATH	P35632	arabidopsiss1
38	324	26.6	209	1	GLOB_T0BAC	P35632	arabidopsiss1
39	320	26.3	227	1	AG17_ARATH	Q3884f1	arabidopsiss1
40	323	26.3	210	1	FBP1_PETHY	003468	petunia_hyb
41	315.5	25.9	231	1	MAD1_PETHY	007472	petunia_hyb
42	308.5	25.3	196	1	FLC_ARATH	Q97567	arabidopsiss1
43	306.5	25.2	227	1	DEFA_ANTHA	P33706	antirrhinum
44	301	24.7	208	1	PIST_ARATH	P48007	arabidopsiss1
45	299	24.5	178	1	AG31_ARATH	Q9fpm7	arabidopsiss1

## ALIGNMENTS

## RESULT 1

ID	AGL8L ARATH	STANDARD;	PRT;	242 AA.
AD	Q38876.			
DT	15-DEC-1998	(Rel. 37, Created)		
DT	15-DEC-1998	(Rel. 37, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Agamous-like MADS box protein AGL8 (Floral homeotic protein AGL8) (FRUITFULL).			
CN	AGL8 OR FUL OR AT5G60910 OR MSL3.3.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatopsida; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=96093419; PubMed=8535133;			
RA	Mandel M.A., Yanofsky M.F.;			
RT	"The Arabidopsis AGL8 MADS box gene is expressed in inflorescence			
RL	meristems and is negatively regulated by APETALA1.";			
RN	Plant Cell 7:1763-1771(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=98162728; PubMed=9501997;			
RA	Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu N.,			
RA	Tabata S.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. III.			
RT	Sequence features of the regions of 1,191,918 bp covered by seventeen			
RL	physically assayed P1 clones.";			
RN	DNA Res. 4:401-414(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RA	Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;			
RT	"The Arabidopsis full length cDNA clones (Rafus) sequenced by the			
RT	SSP consortium (Salk/Stanford/PESC).";			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	FUNCTION, AND TISSUE SPECIFICITY.			
RC	STRAIN=cv. Landsberg erecta;			
RX	MEDLINE=98171466; PubMed=9502732;			
RA	Gu Q., Ferrandiz C., Yanofsky M.F., Martienssen R.;			
RT	"The FRUITFULL MADS-box gene mediates cell differentiation during			
RT	Arabidopsis fruit development.";			
RL	Development 125:1509-1517(1998).			
CC	-1- FUNCTION: Probable transcription factor required for normal			
CC	pattern of cell division, expansion and differentiation during			
CC	morphogenesis of the silique.			
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).			
CC	-1- TISSUE SPECIFICITY: Vascular tissue of cauline leaves, floral			
CC	shoot apex and valves of carpels and fruits.			
CC	-1- INDUCTION: Dramatically up-regulated upon the transition from			
CC	vegetative to reproductive development.			

```
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: U33473; AAA97403.1; -
DR EMBL: AB008269; BAB10640.1; -
DR EMBL: AF386929; AAK62374.1; -
DR EMBL: AY072463; AAL66878.1; -
DR HSSP: P11746; 1MNM.
DR TRANSFAC: T03030; -
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
DR Transcription regulation; DNA-binding; Nuclear protein.
DR DOMAIN 3 57
FT DOMAIN 97 169
SQ SEQUENCE 242 AA; 27536 MW; 516499731EAD82D2 CRC64;

Query Match 100.0%; Score 1218; DB 1; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.8e-74;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGRGRVQLKRIENKINRQVTFKRRSGGLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
DB 1 MGRGRVQLKRIENKINRQVTFKRRSGGLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
OY 61 SCMERILERYDRYLSDKQLVGRDVSQSENWVLEHAKLKARVEVLEKKNRNFGEIDLSTL 120
DB 61 SCMERILERYDRYLSDKQLVGRDVSQSENWVLEHAKLKARVEVLEKKNRNFGEIDLSTL 120
OY 121 SKLEIQLSLERHOLDAAIKSTRSRKNQAMFESISALOKKDALODHNNSLKTIKEREKKTG 180
DB 121 SKLEIQLSLERHOLDAAIKSTRSRKNQAMFESISALOKKDALODHNNSLKTIKEREKKTG 180
OY 181 OEGQLVCCSNSSSVLLPQYCVTSSRDGFVERVGENGASSLTPNSLLPAMMLRPTTT 240
DB 181 OEGQLVCCSNSSSVLLPQYCVTSSRDGFVERVGENGASSLTPNSLLPAMMLRPTTT 240
OY 241 NE 242
DB 241 NE 242

RESULT 2
AGL8_SIGNAL
ID AGL8_SIGNAL STANDARD: PRT; 241 AA.
AC 041274;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL8 homolog (MADS B).
GN AGL8.
OS Sinapis alba (White mustard) (Brassicaceae; Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucots II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE FROM N. A.
RC TISSUE=flower;
```

```
RX MEDLINE=97077349; PubMed=8919916;
RA Menzel G., Apel K., Meizer S.;
RT "Identification of two MADS box genes that are expressed in the
RT apical meristem of the long-day plant Sinapis alba in transition to
RT flowering".
RU Plant J. 9:399-408(1996).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN APICAL MERISTEMS IN TRANSITION
CC TO FLOWERING.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U25695; ABA1525.1; -
DR HSSP: P11746; 1MNM.
DR TRANSFAC: T03168; -
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
DR Transcription regulation; DNA-binding; Nuclear protein.
DR DOMAIN 3 57
FT DOMAIN 97 169
SQ SEQUENCE 241 AA; 27660 MW; 06826CC59E8A94A9 CRC64;

Query Match 91.3%; Score 1112.5; DB 1; Length 241;
Best Local Similarity 91.3%; Pred. No. 2.7e-67;
Matches 221; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

OY 1 MGRGRVQLKRIENKINRQVTFKRRSGGLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
DB 1 MGRGRVQLKRIENKINRQVTFKRRSGGLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
OY 61 SCMERILERYDRYLSDKQLVGRDVSQSENWVLEHAKLKARVEVLEKKNRNFGEIDLSTL 120
DB 61 SCMERILERYDRYLSDKQLVGRDVSQSENWVLEHAKLKARVEVLEKKNRNFGEIDLSTL 120
OY 121 SKLEIQLSLERHOLDAAIKSTRSRKNQAMFESISALOKKDALODHNNSLKTIKEREKKTG 180
DB 121 SKLEIQLSLERHOLDAAIKSTRSRKNQAMFESISALOKKDALODHNNSLKTIKEREKKTG 180
OY 181 OEGQLVCCSNSSSVLLPQYCVTSSRDGFVERVGENGASSLTPNSLLPAMMLRPTTT 240
DB 181 OEGQLVCCSNSSSVLLPQYCVTSSRDGFVERVGENGASSLTPNSLLPAMMLRPTTT 240
OY 241 NE 242
DB 240 NE 241

RESULT 3
AGL8_SOLTU
ID AGL8_SOLTU STANDARD: PRT; 250 AA.
AC 042429;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL8 homolog (POTM1-1).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```



```
OC Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae: euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Superior;
RA MEDLINE=9634393; PubMed=8756601;
RX Kang S.G., Hannapel D.J.;
RT "A novel MADS-box gene of potato (Solanum tuberosum L.) expressed
RT during the early stages of tuberization.";
RL Plant Mol. Biol. 31:379-386(1996).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U23758; AAA92840.1; -.
DR HSSP: P11746; IMNM.
DR TRANSFAC: T03145; -.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TE; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 97 169 K-BOX.
SQ SEQUENCE 250 AA; 28922 MW; EDE37FFFE793DDC4 CRC64;
Query Match 61.0%; Score 743; DB 1; Length 250;
Best Local Similarity 61.8%; Pred. No. 8.8e-43;
Matches 155; Conservative 36; Mismatches 40; Indels 20; Gaps 4;
OY 1 MGRGVQLKRIENKINROVTFESKRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
DB 1 MGRGVQLKRIENKINROVTFESKRSGLLKKAHEISVLCDAEVALIVFSTKGKLFREYAND 60
OY 61 SCMERILERYDYLYSDKQVGRDVSQSENNWYLEHAKLKARVEVLEKKNRMFGEDLSL 120
DB 61 SCMERILERYERYSFARQQLVPTDHTSPGSWTLKAKLRLVLRQKNAHYVGDELSL 120
OY 121 SLKEQLSLEHQAIAIKTSRSRKNQAMFESIALQKKDKALDDHNSLTKIKEREKKTG 180
DB 121 NKEKLQNLHQAIALSKHTRSKKNQMLHESISVLQKQDALDQNNQSKKYEKEKEVA 180
OY 181 QQE--GQLVQCSNSSSVLLPQ-----YCVTSNRDGFVERVYGGENGASGLTE--- 225
DB 181 QONQMDQNHETNSSTFVLPQQLDSPHLGEAVQNTNVYDN-----GEVEGNSSQOQGA 235
OY 226 PRSLPAMMLR 236
DB 236 NNTVMPQWMLR 246
RESULT 4
AGL8_SOLCO STANDARD: PRT: 250 AA.
AC 022328;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
```

```
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL8 homolog.
GN SCM1.
OS Solanum commersonii (Commerson's wild potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae: euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4109;
RN [1]
RP SEQUENCE FROM N.A.
RC Seppanen M.M.;
RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL: AF002666; AAB65161.1; -.
DR HSSP: P11746; IMNM.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TE; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 97 169 K-BOX.
SQ SEQUENCE 250 AA; 28741 MW; C9871403C23ED5D5 CRC64;
Query Match 60.0%; Score 731; DB 1; Length 250;
Best Local Similarity 62.2%; Pred. No. 5.5e-42;
Matches 153; Conservative 39; Mismatches 44; Indels 10; Gaps 3;
OY 1 MGRGVQLKRIENKINROVTFESKRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
DB 1 MGRGVQLKRIENKINROVTFESKRSGLLKKAHEISVLCDAEVALIVFSTKGKLFREYAND 60
OY 61 SCMERILERYDYLYSDKQVGRDVSQSENNWYLEHAKLKARVEVLEKKNRMFGEDLSL 120
DB 61 SCMERILERYERYSFARQQLVPTDHTSPGSWTLKAKLRLVLRQKNAHYVGDELSL 120
OY 121 SLKEQLSLEHQAIAIKTSRSRKNQAMFESIALQKKDKALDDHNSLTKIKEREKKTG 180
DB 121 NKEKLQNLHQAIALSKHTRSKKNQMLHESISVLQKQDALDQNNQSKKYEKEKEVA 180
OY 181 QQE--GQLVQCSNSSSVLLPQ-----YCVTSNRDGFVERVYGGENGASGLTE---PNSIL 230
DB 181 QONQMDQNHETNSSTFVLPQQLDSPHLGEASQNTNVYDNGEVEGNSSQXGAANTVMA 240
OY 231 PAMMLR 236
DB 241 PQMWVR 246
RESULT 5
AGL8_LYCES STANDARD: PRT: 227 AA.
AC 040170;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
```

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DE Agamous-like MADS box protein AGL8 homolog (TM4).
GN TDR.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusteriids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID:4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VENT Cherry; TISSUE=flower;
RX MEDLINE=93251098; PubMed=1688249;
RA Puneli L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer Z.,
RA Lifschitz E.;
RA "The MADS box gene family in tomato: temporal expression during
RT floral development, conserved secondary structures and homology with
RT homeotic genes from Antirrhinum and Arabidopsis.";
RL Plant J. 1:255-266(1991).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: FLOWER-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL: X60757; CAA43169.1; -
DR HSSP: P11746; IMNM.
DR TRANSFAC: T03186; -.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 97 169 K-BOX.
SQ SEQUENCE 227 AA; 26403 MW; 4976195B3BDE53F5 CRC64;
Query Match 58.3%; Score 709.5; DB 1; Length 227;
Best local similarity 72.3%; Pred. No. 1.3e-40;
Matches 141; Conservative 25; Mismatches 24; Indels 5; Gaps 1;
QY 1 MGRGVQLRIENKINROYTFSKRRSGLLKKAHEISVLCDAEYALIVFSSKGLFEYSTD 60
DB 1 MGRGVQLRIENKINROYTFSKRRSGLLKKAHEISVLCDAEYGLVFSKGLFEYAND 60
QY 61 SOMERILEYDYKLSKDLVGRDVSQSEWVLEHAKLKARVEVELEKKNRNFEGDLSL 120
DB 61 SCMERILEYERYSPAELQVLPDHTSPVSWLEHRLKARLEVLQORNRKHVYGEDELSL 120
QY 121 SLKEQSLLEHODAAIKSIRSRKNQAMFESISALOKKDKALDHNNSLLKTIKERKKNG 180
DB 121 SMKEQNLNEHODSALKTRSRKNQMLHESISVLYOKKDRALDEONNOLSKVAKEREKSAQ 180
QY 181 QOEGQLVQCSNNSV 195
DB 181 QISG-----INSSL 190

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DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Floral homeotic protein APTALAI (AGL7 protein).
GN APL OR AGL7 OR ATIG69120 OR FAN2.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=93063372; PubMed=1359429;
RA Mandel M.A., Gustafson-Brown C., Savidge B., Yanofsky M.F.;
RT "Molecular characterization of the Arabidopsis floral homeotic gene
RT APTALAI.";
RL Nature 360:273-277(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujil C.Y.,
RA Gali J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malt R., Marzilli A.,
RA Millscher J., Miranda M., Nguyen M., Niernm W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
RN [3]
RP SEQUENCE OF 1-251 FROM N.A.
RC STRAIN=Various strains;
RX MEDLINE=21969421; PubMed=11973317;
RA Olsen K.M., Womack A., Garrett A.R., Suddith J.I., Putuganan M.D.;
RT "Contrasting evolutionary forces in the Arabidopsis thaliana floral
RT developmental pathway.";
RL Genetics 160:1641-1650(2002).
CC -1- FUNCTION: CONTROLS FLORAL MERISTEM IDENTITY. IS ALSO REQUIRED FOR
CC NORMAL DEVELOPMENT OF SEPAL AND PETALS. IS REQUIRED FOR THE
CC TRANSITION OF AN INFLORESCENCE MERISTEM INTO A FLORAL MERISTEM.
CC INTERACTS WITH LEAFY.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN YOUNG FLOWER PRIMORDIA, LATER
CC BECOMES LOCALIZED TO SEPAL AND PETALS.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL: Z16421; CAA78909.1; -
DR EMBL: AC008262; AAF27070.1; -
DR EMBL: AF466771; AAM28447.1; -
DR EMBL: AF466772; AAM28448.1; -
DR EMBL: AF466773; AAM28449.1; -

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DR EMBL: AF466774; AAM28450.1; -
DR EMBL: AF466775; AAM28451.1; -
DR EMBL: AF466776; AAM28452.1; -
DR EMBL: AF466777; AAM28453.1; -
DR EMBL: AF466778; AAM28454.1; -
DR EMBL: AF466779; AAM28455.1; -
DR EMBL: AF466780; AAM28456.1; -
DR EMBL: AF466781; AAM28457.1; -
DR EMBL: AF466782; AAM28458.1; -
DR EMBL: AF466783; AAM28459.1; -
DR EMBL: AF466784; AAM28460.1; -
DR EMBL: AF466785; AAM28461.1; -
DR HSSP: P11746; 1NMN.
DR TRANSFAC: T01775; -
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRP-TP; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS.1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR Transcription regulation; DNA-binding; Activator; Nuclear protein;
KW Developmental protein; Polymorphism.
FT DOMAIN 3 57 MADS.
FT VARIANT 97 169 S->P (IN STRAIN CV. CHI-1).
FT VARIANT 93 93 M->T (IN STRAIN CV. BLA-1).
FT VARIANT 99 99 K->R (IN STRAIN CV. CHI-1).
FT VARIANT 100 100 A->T (IN STRAIN CV. LER).
FT VARIANT 120 120 M->P (IN STRAIN CV. JL-1).
FT VARIANT 125 125 L->P (IN STRAIN CV. BLA-1).
FT VARIANT 166 166 S->G (IN STRAIN CV. JL-1).
FT VARIANT 212 212 L->P (IN STRAIN CV. CHI-1).
FT VARIANT 233 233 A->V (IN STRAIN CV. CHI-1).
FT CONFLICT 184 184 E->G (IN REF. 3; AAM28458).
FT CONFLICT 236 236 MISSING (IN REF. 1).
SQ SEQUENCE 256 AA; 30182 MW; 01E26DE18CE3478C CRC64;
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Query Match 54.4%; Score 662.5; DB 1; Length 256;
Best Local Similarity 65.8%; Pred. No. 2e-37;
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;
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OY 1 MGRGRVQLKRIENKINRQYTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
DB 1 MGRGRVQLKRIENKINRQYTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
OY 61 SCMERILERYDRYLYSDKQVGRDVVSQSENWYLEHAKLKAARVEYLEKKNRNPMDGEDLSL 120
DB 61 SCMERILERYERYSYAERQLIAPESDVNTNMSMEYNRKAKITELLERNRHYLGEDLOAM 120
OY 121 SKELOSLERHOLDATKISRKRNOAMFESISALOKKDALDHNNSLLKTKIKEREK-KT 179
DB 121 SKELOSLERHOLDATKISRKRNOAMFESISALOKKDALDHNNSLLKTKIKEREK 180
OY 180 GQGE--GGLVQCSNSSSVLLPQ 199
DB 181 AQQEQMDQDQNGHNMPPRPQ 202

RESULT 7
AP1_SINAL STANDARD: PRT; 254 AA.
AC 041276;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Floral homeotic protein APETALA1 (MADS C).
GN AP1.
OS Sinapis alba (White mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Sinapis.
```

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OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=flower.
RX MEDLINE=95334514; PubMed=7610185;
RA Menzel G., Apel R., Melzer S.;
RT "Isolation and analysis of SamDS C, the APETALA 1 cDNA homolog from
   mustard."
RL Plant Physiol. 108:853-854(1995).
CC -I- FUNCTION: CONTROLS FLORAL MERISTEM IDENTITY. IS ALSO REQUIRED FOR
CC NORMAL DEVELOPMENT OF SEPAL AND PETALS. IS REQUIRED FOR THE
CC INTERACTION OF AN INFLUORESCENCE MERISTEM INTO A FLORAL MERISTEM.
CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -I- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -I- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC -----
DR EMBL: X81480; CAA57233.1; -
DR HSSP: P11746; 1NMN.
DR TRANSFAC: T03169; -
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRP-TP; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS.1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR Transcription regulation; DNA-binding; Activator; Nuclear protein;
KW Developmental protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 97 169 K-BOX.
SQ SEQUENCE 254 AA; 29918 MW; 187FEEDE51BEF743 CRC64;
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Query Match 53.9%; Score 656; DB 1; Length 254;
Best Local Similarity 64.1%; Pred. No. 5.3e-37;
Matches 127; Conservative 38; Mismatches 33; Indels 0; Gaps 0;
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OY 1 MGRGRVQLKRIENKINRQYTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
DB 1 MGRGRVQLKRIENKINRQYTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
OY 61 SCMERILERYDRYLYSDKQVGRDVVSQSENWYLEHAKLKAARVEYLEKKNRNPMDGEDLSL 120
DB 61 SCMERILERYERYSYAERQLIAPESDVNTNMSMEYNRKAKITELLERNRHYLGEDLOAM 120
OY 121 SKELOSLERHOLDATKISRKRNOAMFESISALOKKDALDHNNSLLKTKIKEREKKTG 180
DB 121 SKELOSLERHOLDATKISRKRNOAMFESISALOKKDALDHNNSLLKTKIKEREK 180
OY 181 QOEGQLVQCSNSSSVLLP 198
DB 181 AQQEQMDQDQNGHNMPPRP 198

RESULT 8
CMB1_DIACA STANDARD: PRT; 233 AA.
AC 039685;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE MADS box protein CMB1.
GN CMB1.
```

OS Dianthus caryophyllus (Carnation) (Clove pink).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.  
OX NCBI\_TaxID=3570;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Scania; TISSUE=Petal;  
RA Baudinette S.C.; Savin K.W.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.  
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CC -----  
DR EMBL: L40404; AAA62761.1; -  
DR HSSP: P11746; 1MNM.  
DR TRANSFAC: T03060; -  
DR InterPro: IPR002487; TF\_Kbox.  
DR InterPro: IPR002100; TF\_MADSbox.  
DR Pfam: PF00319; SRF-TF; 1.  
DR Pfam: PF01486; K-box; 1.  
DR PRINTS: PR00404; MADSDOMAIN.  
DR SMART: SM00432; MADS; 1.  
DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
DR PROSITE: PS50066; MADS\_BOX\_2; 1.  
DR Transcription regulation; DNA-binding; Nuclear protein.  
FT DOMAIN 3 58 MADS.  
FT DOMAIN 96 168 K-BOX.  
SQ SEQUENCE 233 AA; 26888 MW; CB8765618466151A CRC64;  
  
Query Match 41.8%; Score 509; DB 1; Length 233;  
Best Local Similarity 44.3%; Pred. No. 2.7e-27;  
Matches 109; Conservative 45; Mismatches 68; Indels 24; Gaps 3;  
  
QY 1 MGRGRVQLKRIENKINRQYTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
DB 1 MGRGRVELKRIENKINRQYTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYCS 60  
QY 61 SCMERILERYDRLYSDKQVGRDVSQSENMVLEHAKIKARVLEKKNRNMGGEDLSL 120  
DB 61 SCMNKLTLEKQKCSYGSLE-TSQPSKETESSYQVEYIKLAKAVYLQSRNRLGEDLGEL 119  
QY 121 SKELOSLERHOLDAAIKSIRSRKNQAMFESISALOKKDALODHNNSLKIKE----- 174  
DB 120 SKTELEQLERQDGLSKQYRSIKTYQMDQLDLOKKEKLEFESNALKTLESCASFR 179  
QY 175 -----REKKTGGQEGOLVQCCSNSSSVLLPQYCVTSRRDGFVERVGGENGASSLTPE 229  
DB 180 PMNDVROPDGFEPLPLPCNNNLOI-----GYNEATQDOMNATTAQVNHGF 227  
QY 230 LPAMML 235  
DB 228 AGGMWL 233

OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91160981; PubMed=1672119;  
RA Ma H., Yanofsky M.F., Meyerowitz E.M.;  
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral  
RT homeotic and transcription factor genes";  
RL Genes Dev. 5:484-495(1991).  
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING FLOWER DEVELOPMENT.  
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: M5551; AAA32732.1; -  
DR PIR: B39534; B39534.  
DR HSSP: P11746; 1MNM.  
DR TRANSFAC: T03024; -  
DR InterPro: IPR002487; TF\_Kbox.  
DR InterPro: IPR002100; TF\_MADSbox.  
DR Pfam: PF00319; SRF-TF; 1.  
DR Pfam: PF01486; K-box; 1.  
DR PRINTS: PR00404; MADSDOMAIN.  
DR SMART: SM00432; MADS; 1.  
DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
DR PROSITE: PS50066; MADS\_BOX\_2; 1.  
DR Transcription regulation; DNA-binding; Nuclear protein.  
FT DOMAIN 3 57 MADS.  
FT DOMAIN 97 169 K-BOX.  
SQ SEQUENCE 248 AA; 28454 MW; 8B70DD4512AC906B CRC64;  
  
Query Match 39.8%; Score 484.5; DB 1; Length 248;  
Best Local Similarity 44.0%; Pred. No. 1.2e-25;  
Matches 109; Conservative 46; Mismatches 80; Indels 13; Gaps 4;  
  
QY 1 MGRGRVQLKRIENKINRQYTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
DB 1 MGRGRVELKRIENKINRQYTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYCS 60  
QY 61 SCMERILERYDRLYSDKQVGRDVSQSENMVLEHAKIKARVLEKKNRNMGGEDLSL 120  
DB 61 SNNKLTLDKQKCSYGSIEENKPAKELNYSREYIKLKGRENNLRQORNLGDELPL 120  
QY 121 SKELOSLERHOLDAAIKSIRSRKNQAMFESISALOKKDALODHNNSLKIKE-----RE 176  
DB 121 NSKTELEQLERQDGLSKQYRSIKTYQMDQLDLOKKEKLEFESNALKTLESCASFR 180  
QY 177 KKTGGQEG--QVQCSN-----SSSVLLPQYCVTSRRDGFVERVGGENGASSLTPE---N 227  
DB 181 HHMGWEGEGEUNVYAHQAOAGGILQPLECNPTLQMGYDNVCSQITATTAQAOAGCN 240  
QY 228 SLIPAMML 235  
DB 241 GYIPGMWL 248

RESULT 9  
AGL2\_ARATH  
ID AGL2\_ARATH STANDARD: PRT: 248 AA.  
AC P29382;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Agamous-like MADS box protein AGL2.  
GN AGL2.

RESULT 10  
AGL9\_PETHY  
ID AGL9\_PETHY STANDARD: PRT: 241 AA.  
AC Q03489;

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DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AG19 homolog (Floral homeotic protein
DE FBP2) (Floral binding protein 2).
GN FBP2.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxId=4102;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93005737; PubMed=1356537;
RA Angenot G.C., Busscher M., Franken J., Mol J.N.M., van Tunen A.J.;
RT "Differential expression of two MADS box genes in wild-type and
RT mutant Petunia flowers.";
RL Plant Cell 4:983-993(1992).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Angenot G.C.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear..
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
DR EMBL: M91666; AAA86854.1;
DR PIR: J01690; J01690.
DR HSSP: P11746; 1MNM.
DR TRANSFAC: T03093;
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS_1;
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 98 170 K-BOX.
SQ SEQUENCE 241 AA; 27562 MW; B575B9468D310BB CRC64;
Query Match 38.8%; Score 472; DB 1; Length 241;
Best Local Similarity 42.6%; Pred. No. 7.8e-25;
Matches 107; Conservative 47; Mismatches 69; Indels 28; Gaps 6;
QY 1 MGRGVQLKRIENKINROYTEKRSKGLKKAHEISVLCDAVALIVSSKKLFYEYSTD 60
DB 1 MGRGVQLKRIENKINROYTEKRSKGLKKAHEISVLCDAVALIVSSNRKLFYFSS 60
OY 61 SEMEILERYDRYLYSDKOLVGRDVSSENNWL----EHAKKARVEVLEKKRNFMGD 116
DB 61 SEMKLTLERYQKCNVGAPE---TNISTREALEISOOEYELIKAKAYEALORSORNLGHD 117
OY 117 IDSLSLKELOSLEHOLDAAIKSIRSRKQAMFESISALOKKDALODHNNSLLKRIKERE 176
DB 118 LQPLNSKELESEROLDMSLKQIRSTRQULMDOLQDKRKEHALNEANRFLKQKLGESS 177
OY 177 KRTGOOEGLVQCSNSSLVLPQYCVTSSRDGFVE-----RVGGEN-----GGASL 223
DB 178 TLNLQWQ-----QNAODVGVGRQATQTOGDGFHPLBCEPTLQIGYONDPTTVGAG-- 229

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QY 224 TEPNLSLPAMM 234
DB 230 PSVNNVMAGWL 240
RESULT 11
AGL4_ARATH STANDARD: PRT; 250 AA.
AC P29384;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL4.
GN AGL4 OR AT3G02310 OR F14P3.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160981; PubMed=1672119;
RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral
RT homeotic and transcription factor genes.";
RL Genes Dev. 5:484-495(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansgore W., Unselid M.,
RA Fattmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Griuell L.A., Maché R., Pulgomech P.,
RA De Simone V., Cholise N., Artiguenave F., Robert C., Brotlier P.,
RA Wincker P., Catolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs N., Benes V.,
RA Wurnbach E., Drzonek H., Erle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nykatuna G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordiek G.,
RA Reichelt J., Scharte M., Schoen O., Barques M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchem D.,
RA Cooke R., Lande M., Berger-Laurio C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacubeta E.,
RA Monfort A., Argillou A., Flores M., Lignori R., Vitale D.,
RA Mannhaupt G., Haese D., Schoof H., Rudd S., Zaccaria P., Meves H.-M.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T.H., Rizzo M., Walts A., Uterback T., Fujil C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Mllitscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asanuma E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shindo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING FLOWER DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
DR EMBL: M55552; AAA32734.1; -
DR EMBL: AC009755; AAF02125.1; -
DR PIR: D39534; D39534.
DR HSSP: P11746; 1MNM.
DR TRANSFAC: T03027; -
DR InterPro: IPR002467; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRP-TE; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS.1
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 MADS.
FT DOMAIN 97 169 K-BOX.
SQ SEQUENCE 250 AA; 28577 MW; 53136FE263389943 CRC64;

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Query Match 38.1%; Score 463.5; DB 1; Length 250;
Best Local Similarity 41.1%; Pred. No. 3e-24;
Matches 109; Conservative 40; Mismatches 71; Indels 45; Gaps 5;

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OY 1 MGRGRVQLRKRIENKINRQVTFESRRSGGLKKAHISVLCDAEVALIVSSSGKLFESTD 60
DB 1 MGRGRVQLRKRIENKINRQVTFESRRSGGLKKAHISVLCDAEVALIVSSSGKLFESTD 60
OY 61 SCMERILTERDRLYSADKOLVGRDVSQSENVWLEHAFLKARVLEKKNRNGEDLDST 120
DB 61 SMMLKLELYKQCSYGSIEVNNKPAKELENSYREYLKLRKYENLRQCNLGEDGGL 120
OY 121 SKKELOSLHOLDAAIKSTRSRKNQAFESISALOKKALQDHNNSLKKRIE----R 175
DB 121 SKKELOSLHOLDAAIKSTRSRKNQAFESISALOKKALQDHNNSLKKRIE----R 175
OY 121 NSKELEQLEROLDGSLKQVRCIKTYMLDQLSDLOGKEHLLDANRALSKLEDMIGVRH 180
DB 121 NSKELEQLEROLDGSLKQVRCIKTYMLDQLSDLOGKEHLLDANRALSKLEDMIGVRH 180
OY 176 EKKTGQEG-----QLYOC-----SNSSVLLPQCVYSSRGEV 210
DB 181 HIIGGWEGBGDOONLIVGHPQASGLYSLECDPLTQIGYSHPVCSQMAVT----- 233
OY 211 ERYVGENGGASSLTPEPNSLLPAMWL 235
DB 234 --VQGS-----QQNGYIPGMWL 250

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RESULT 12
AGL9_ARATH STANDARD; PRT; 251 AA.
AC AG2456;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9.
GN AGL9 OR AT1G24260 OR F316.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RA Mandel M.A., Yanofsky M.F.;
RT "The Arabidopsis AGL9 MADS box gene is expressed in young flower
primordia.";
RL Sex. Plant Reprod. 11:22-28(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA MEDLINE=21016719; PubMed=1130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

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RA Dunn P., Elgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gull J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malt R., Marzali A.,
RA Maltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana.";
RL Nature 408:816-820(2000).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
DEVELOPMENT AND FLORAL ORGANOGENESIS.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING FLOWER DEVELOPMENT
WITHIN PETALS, STAMENS, AND CARPELS.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC EMBL: AF015552; AAB67832.1; -
CC EMBL: AC002396; AAC00586.1; -
CC HSSP: P11746; 1MNM.
CC TRANSFAC: T03027; -
CC InterPro: IPR002467; TF_Kbox.
CC InterPro: IPR002100; TF_MADSbox.
CC Pfam: PF00319; SRP-TE; 1.
CC Pfam: PF01486; K-box; 1.
CC PRINTS: PR00404; MADSDOMAIN.
CC SMART: SM00432; MADS.1.
CC PROSITE: PS00350; MADS_BOX_1; 1.
CC PROSITE: PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 MADS.
FT DOMAIN 100 172 K-BOX.
SQ SEQUENCE 251 AA; 29066 MW; 0057CABD3F1AFC40 CRC64;

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Query Match 37.8%; Score 461; DB 1; Length 251;
Best Local Similarity 41.0%; Pred. No. 4.4e-24;
Matches 107; Conservative 47; Mismatches 75; Indels 32; Gaps 6;

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OY 1 MGRGRVQLRKRIENKINRQVTFESRRSGGLKKAHISVLCDAEVALIVSSSGKLFESTD 60
DB 1 MGRGRVQLRKRIENKINRQVTFESRRSGGLKKAHISVLCDAEVALIVSSSGKLFESTD 60
OY 61 SCMERILTERDRLYS-----DKOLVGRDVSQSENVWLEHAFLKARVLEKKNRNGE 113
DB 61 SSMKLELYKQCSYGSIEVNNKPAKELENSYREYLKLRKYENLRQCNLGEDGGL 116
OY 114 GEDLDSLSEKLOSLHOLDAAIKSTRSRKNQAFESISALOKKALQDHNNSL----- 168
DB 117 GEDLGPLSTKLESLEROLDGSLKQVRCIKTYMLDQLSDLOGKEHLLDANRALSKLE 176
OY 169 -----LKKIKERKKTGGQEGQLVQCSNSSVLLPQCVYSSRGEFVERVGENGCA 220
DB 177 DGXOMPLQNLNPNQEEVDHGRHHNQ--QOHSQAFQPLCEEPILQIGYQGOQGMGAGP 234
OY 221 SSLEPNSLLPAMWLPTTN 241
DB 235 S-----VNNYMLGWL--PYDTN 249

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RESULT 13
AGL9_SINAL
ID AGL9_SINAL STANDARD: PRT: 254 AA.
AC 004067;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9 homolog (MADS D).
GN AGL9.
OS Sinapis alba (white mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=flower;
RX MEDLINE=97390682; PubMed=9247539;
RA Borhomme F., Sommer H., Bernier G., Jacquard A.;
RT "Characterization of SAMADS D from Sinapis alba suggests a dual
RT function of the gene: in inflorescence development and floral
RT organogenesis.";
RL Plant Mol. Biol. 34:573-573(1997).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
CC DEVELOPMENT AND FLORAL ORGANOGENESIS.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity)
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y08626; CAA69916.1; -.
DR HSSP: P11746; 1MM.
DR TRANSFAC: T03170; -.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 100 172 K-BOX.
SQ SEQUENCE 254 AA; 29603 MW; EDD65155060BFD46 CRC64;

Query Match 36.9%; Score 449.5; DB 1; Length 254;
Best local similarity 39.3%; Pred. No. 2.6e-23;
Matches 103; Conservative 53; Mismatches 75; Indels 31; Gaps 6;

QY 1 MGRGVOLKRIENKINROVYTSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
DQ 1 MGRGVOLKRIENKINROVYTSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
DB 1 MGRGVOLKRIENKINROVYTSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
QY 61 SCMERILERYRILYS-----DKOLVGRDVSSENNVLEHAKIKAVEYLEKKRNFM 113
DQ 61 SCMERILERYRILYS-----DKOLVGRDVSSENNVLEHAKIKAVEYLEKKRNFM 113
DB 61 SCMERILERYRILYS-----DKOLVGRDVSSENNVLEHAKIKAVEYLEKKRNFM 113
QY 114 GEDDLSLKELOSLEHOLDIAIKSIRSKNOAMPESISALOKKADODNNNSLTKTI- 172
DQ 114 GEDDLSLKELOSLEHOLDIAIKSIRSKNOAMPESISALOKKADODNNNSLTKTI- 172
DB 117 GEDDLSLKELOSLEHOLDIAIKSIRSKNOAMPESISALOKKADODNNNSLTKTI- 176
QY 173 -----KERERKTKGOEGOLVQCSNSSSVLLPQYCVTSSRDGFVERVGENG 219
DQ 173 -----KERERKTKGOEGOLVQCSNSSSVLLPQYCVTSSRDGFVERVGENG 219
DB 173 -----KERERKTKGOEGOLVQCSNSSSVLLPQYCVTSSRDGFVERVGENG 219
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DB 177 DGQMPLOLNPQEDHVDYGRHDDQOQONSH-HAFQPLECEPILQMGY---QGQDDHG 232
QY 220 ASSLTPEPNSLDPAMMLRPPTTN 241
DQ 220 ASSLTPEPNSLDPAMMLRPPTTN 241
DB 233 MEAGSENNYMLGWL--PYDTN 252

RESULT 14
AGL9_LYCES
ID AGL9_LYCES STANDARD: PRT: 224 AA.
AC 042464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9 homolog (TMS).
GN TMS.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VENT Cherry; TISSUE=flower;
RX MEDLINE=93251098; PubMed=1688249;
RA Punell L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer Z.,
RA Litschitz E.;
RT "The MADS box gene family in tomato: temporal expression during
RT floral development, conserved secondary structures and homology with
RT homeotic genes from Antirrhinum and Arabidopsis.";
RL Plant J. 1:255-266(1991).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
CC DEVELOPMENT AND FLORAL ORGANOGENESIS (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: FLOWER-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X60758; CAA43170.1; -.
DR EMBL: X60480; CAA43010.1; -.
DR HSSP: P11746; 1MM.
DR TRANSFAC: T03187; -.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 98 170 K-BOX.
SQ SEQUENCE 224 AA; 25999 MW; 51D10D30867D0067 CRC64;

Query Match 36.9%; Score 449; DB 1; Length 224;
Best local similarity 48.7%; Pred. No. 2.4e-23;
Matches 96; Conservative 41; Mismatches 40; Indels 20; Gaps 5;

QY 1 MGRGVOLKRIENKINROVYTSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
DQ 1 MGRGVOLKRIENKINROVYTSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
DB 1 MGRGVOLKRIENKINROVYTSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
QY 61 SCMERILERYRILYS-----SDKOLVGRDVSSENNVLEHAKIKAVEYLEKKRNFM 113
DQ 61 SCMERILERYRILYS-----SDKOLVGRDVSSENNVLEHAKIKAVEYLEKKRNFM 113
DB 61 SCMERILERYRILYS-----SDKOLVGRDVSSENNVLEHAKIKAVEYLEKKRNFM 113
```



Db 61 SSMLETLLEYQKCNKINROVTFESKRRSGLLKKAHEISVLCDAEVALIFVSSKGLFEYSTD 114  
 QY 114 GEDLDSLSEKELQSLHOLDAAIKSIRSRKNQAMFESISALOKKDALODHNSLKKIKERBK 173  
 Db 115 GEDLDPINSEKELQSLHOLDAAIKSIRSRKNQAMFESISALOKKDALODHNSLKKIKERBK 174  
 QY 174 EREKKTGOEGOLVOCSS 190  
 Db 175 E-----GSOLN--LQCS 184

## RESULT 15

AGL9\_ARADE STANDARD: PRT; 250 AA.

AC Q38694;  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Agamous-like MADS box protein AGL9 homolog (OM1).  
 OS Arabidopsis thaliana (Arabidopsis).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;  
 CC Epidendroideae; higher Epidendroideae; Vandaceae; Aeridinae;  
 CC Aechmea x Vanda.  
 CX NCBI\_TaxID=29714;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94072738; PubMed=8251643;  
 RA Lu Z.X., Wu M., Loh C.S., Yeong C.Y., Goh C.J.;  
 RT "Nucleotide sequence of a flower-specific MADS box cDNA clone from  
 orchid.";  
 RL Plant Mol. Biol. 23:901-904(1993).  
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE  
 DEVELOPMENT AND FLORAL ORGANOGENESIS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND WEAKLY IN SEPAL BUT  
 NOT IN THE COLUMN (GYNOSTEMIUM).  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN MATURE FLOWERS AND NOT IN YOUNG  
 DEVELOPING INFLORESCENCES OR YOUNG FLORAL BUDS.  
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
 FACTORS  
 CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X69107; CAA48859.1; -.  
 DR HSSP: P11746; IMNM.  
 DR TRANSFAC: T03114; -.  
 DR InterPro: IPR002487; TF\_Kbox.  
 DR InterPro: IPR002100; TF\_MADSbox.  
 DR Pfam: PF00319; SRF-TF; 1.  
 DR Pfam: PF01486; K-box; 1.  
 DR PRINTS: PRO0404; MADSDOMAIN.  
 DR SMART: SM00432; MADS; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE: PS50066; MADS\_BOX\_2; 1.  
 KM Transcription regulation; DNA-binding; Nuclear protein.  
 FT DOMAIN 3 57 MADS.  
 FT DOMAIN 96 168 K-BOX.  
 SQ SEQUENCE 250 AA; 28770 MW; 01EF94DADC499C41 CRC64;

Query Match 36.6%; Score 446; DB 1; Length 250;

Best Local Similarity 38.9%; Pred. No. 4.3e-23;  
 Matches 96; Conservative 56; Mismatches 77; Indels 18; Gaps 4;

QY 1 MGRGVQLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIFVSSKGLFEYSTD 60

Db 1 MGRGVQLKRIENKINROVTFESKRRSGLLKKAHEISVLCDAEVALIFVSSKGLFEYSTD 60  
 QY 61 SCMERLIERDRYLYS--DKOLVGRDVSOSEMMVLEHAKLKVAVLLEKKNRNFGEGLD 116  
 Db 61 TSMLEKLEKTYQKCNKINROVTFESKRRSGLLKKAHEISVLCDAEVALIFVSSKGLFEYSTD 117  
 QY 119 SLSEKELQSLHOLDAAIKSIRSRKNQAMFESISALOKKDALODHNSLKKIKERBK 178  
 Db 118 PLGSKLEQLERQDSSLSLQIRSTRQFMQLDQLDQREQLCEANNTLKRFEESQA 177  
 QY 179 TGOQ-----EGOLVOCSSSSVLLPOCYTSSRDGVEVERGEGNGCASSLTPN 227  
 Db 178 NDOQVMDPSNTHAVGYGROPQOHGFAFYHPLCEPTLQIGYHSDITMATATASTVN--N 235  
 QY 228 SLPPAM 234  
 Db 236 YMPGWL 242

Search completed: January 27, 2003, 12:38:22  
 Job time : 13 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2003, 12:37:27 : Search time 19 Seconds  
(without alignments)  
1224.449 Million cell updates/sec

Title: US-09-981-087a-2

Perfect score: 1218

Sequence: 1 MGRGRVQLKRIENKINRQVT.....LTPDNSLLPAMMLRPTTNE 242

Scoring table:

BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1218	100.0	242	2 S71208	MADS box protein A
2	743	61.0	250	2 T07100	MADS box protein h
3	731	60.0	250	2 T07902	MADS box protein h
4	709.5	58.3	227	2 S23730	MADS box protein T
5	683	56.1	248	2 S20886	MADS box protein s
6	662.5	54.4	256	2 S27109	MADS box protein A
7	656	53.9	254	2 S52236	MADS box protein A
8	621.5	51.0	251	2 T14436	MADS box protein h
9	610.5	50.1	273	2 T03410	MADS box protein h
10	575.5	47.2	228	2 T14737	MADS box protein -
11	548	45.0	150	2 T14457	MADS box protein h
12	509	41.8	233	2 T10714	MADS box protein c
13	500	41.1	245	2 T09569	MADS box protein M
14	497.5	40.8	261	2 S51935	MADS box protein M
15	497.5	40.8	261	2 T09603	MADS box protein h
16	497	40.8	242	2 T10486	MADS box protein -
17	497	40.8	242	2 T09571	MADS box protein M
18	491.5	40.4	246	2 T17023	MADS box protein 1
19	491	40.3	257	2 S53306	MADS box protein A
20	484.5	39.8	248	2 B39534	MADS box protein A
21	476	39.1	249	2 T04335	MADS box protein -
22	473	38.8	225	2 T04170	MADS box protein -
23	470.5	38.6	225	2 T04168	MADS box protein -
24	470	38.6	249	2 T04307	M79 protein - rice
25	467	38.3	231	2 T14801	MADS box protein M
26	466	38.3	247	2 S78015	MADS box protein D
27	466	38.3	259	2 T04169	MADS box protein D
28	464.5	38.1	262	2 T51409	MADS box protein A
29	463.5	38.1	242	2 S71757	MADS box protein D

30	463.5	38.1	250	2 D39534	MADS box protein A
31	462	37.9	243	2 S71756	MADS box protein D
32	461	37.8	251	2 T00656	MADS box protein A
33	460	37.8	224	2 J01690	MADS box protein f
34	456	37.4	250	2 T04167	MADS box protein -
35	455.5	37.4	255	2 T03408	MADS box protein -
36	454	37.3	255	2 T03398	MADS box protein -
37	453.5	37.2	247	2 T06543	MADS box protein -
38	449.5	36.9	254	2 T10467	MADS box protein D
39	449	36.9	224	2 S23728	MADS box protein T
40	446	36.6	250	2 S40405	MADS box protein O
41	442	36.3	252	2 F39534	MADS box protein O
42	432.5	35.5	258	2 S57793	floral homeotic pr
43	427	35.1	244	2 T47904	MADS box protein A
44	420	34.5	219	2 S46526	MADS box protein A
45	416.5	34.2	248	2 T03592	MADS box protein m floral homeotic pr

## ALIGNMENTS

```
RESULT 1
S71208
MADS box protein AGL8 - Arabidopsis thaliana
N:Alternate names: agamous-like protein 8
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 24-Sep-1999
C:Accession: S71208
R:Mandel, M.A.; Yanofsky, M.F.
submitted to the EMBL Data Library, August 1995
A:Description: The Arabidopsis AGL8 MADS box gene is expressed in inflorescence meris
A:Reference number: S71208
A:Accession: S71208
A:Molecule type: mRNA
A:Residues: 1-242 <MAN>
A:Cross-references: EMBL:U33473; NID:g1004364; PIDN:AAA97403.1; PID:g1004365
C:Genetics:
A:Gene: AGL8
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C:Keywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match          100.0%  Score 1218; DB 2; Length 242;
Best Local Similarity 100.0%  Pred. No. 5.2e-73;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGRVQLKRIENKINRQVTFSKRRSGLKKAHEISVLCDAEVALTFSSKGLPEYSTD 60
    |||||||
DB 1 MGRGRVQLKRIENKINRQVTFSKRRSGLKKAHEISVLCDAEVALTFSSKGLPEYSTD 60

QY 61 SCMERILERYDRLYSKQOLVGRDVSQSENWYLEHAKLKARVEVLEKKNRMFGEDLDSL 120
    |||||||
DB 61 SCMERILERYDRLYSKQOLVGRDVSQSENWYLEHAKLKARVEVLEKKNRMFGEDLDSL 120

QY 121 SLKEIQLSEHOLDAAIKTSIRSRKKNQAMFESISALOKKDALDHNHNSLTKIKEREKKTG 180
    |||||||
DB 121 SLKEIQLSEHOLDAAIKTSIRSRKKNQAMFESISALOKKDALDHNHNSLTKIKEREKKTG 180

QY 181 QOEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGENGASSLTPEPNSLLPAMMLRPTTT 240
    |||||||
DB 181 QOEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGENGASSLTPEPNSLLPAMMLRPTTT 240

QY 241 NE 242
    ||
DB 241 NE 242

RESULT 2
T07100
MADS box protein homolog POTM1-1 - potato
C:Species: Solanum tuberosum (potato)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C:Accession: T07100
```



A:Cross-references: EMBL:X63701; NID:g16051; PIDN:CAA45228.1; PID:g16052  
C:Genetics:  
A:Gene: sga  
A:Introns: 62/2; 88/3; 110/2; 143/3; 157/3; 171/3; 215/2  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C:Keywords: DNA binding; nucleus; transcription regulation  
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 56.1%; Score 683; DB 2; Length 248;  
Best Local Similarity 70.3%; Pred. No. 6.4e-38;  
Matches 128; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MGRGVOLKRIENKINRQVTFSSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINRQVTFSSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Qy 61 SCMERILERYRYLYSDKOLVGRDVSQSEBNVLEHAKEVLEKKNRMFGEDLDSL 120  
Db 61 SCMERILEKERYRYFAEROLVSNFQSPANWLTLEYSKRLKARIELLQRNHRHVMGEDLDSM 120

Qy 121 SLKELOSLEHOLDAAIKSIRSRKNQAMFESTSALOKKKAODHNNLSLKIKEREKKTG 180  
Db 121 SLKELOSLEHOLDPALKNIRKKNOLYDSTSELOHKEKAIOEONTMLAKRIKEKEA 180

Qy 181 QQ 182  
Db 181 QQ 182

#### RESULT 6

MADS box protein Ap1 - Arabidopsis thaliana

N:Alternate names: floral homeotic protein Ap1

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 24-Sep-1999

C:Accession: S27109; S36597

R:Mandel, M.A.; Gustafson-Brown, C.; Savidge, B.; Yanofsky, M.F.

Nature 360, 273-277, 1992

A:Title: Molecular characterization of the Arabidopsis floral homeotic gene APETALA1.

A:Reference number: S27109; MUID:93063372; PMID:1359429

A:Accession: S27109

A:Molecule type: mRNA

A:Residues: 1-256 <MAN>

A:Cross-references: EMBL:Z16421; NID:g16161; PIDN:CAA78909.1; PID:g16162

A:Note: 27-Asp was also found

R:Yanofsky, M.F.

submitted to the EMBL Data Library, October 1992

A:Reference number: S36597

A:Accession: S36597

A:Molecule type: mRNA

A:Residues: 1-235,237-256 <YAN>

A:Cross-references: EMBL:Z16421; NID:g16161; PIDN:CAA78909.1; PID:g16162

C:Genetics:

A:Map position: 1

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C:Keywords: DNA binding; nucleus; transcription regulation

F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 54.4%; Score 662.5; DB 2; Length 256;  
Best Local Similarity 65.8%; Pred. No. 1.5e-36;  
Matches 133; Conservative 33; Mismatches 33; Indels 3; Gaps 2;

Qy 1 MGRGVOLKRIENKINRQVTFSSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINRQVTFSSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60

Qy 61 SCMERILERYRYLYSDKOLVGRDVSQSEBNVLEHAKEVLEKKNRMFGEDLDSL 120  
Db 61 SCMERILEKERYRYFAEROLVSNFQSPANWLTLEYSKRLKARIELLQRNHRHVMGEDLDSM 120

Qy 121 SLKELOSLEHOLDAAIKSIRSRKNQAMFESTSALOKKKAODHNNLSLKIKEREK-KT 179  
Db 121 SKRELONLEOQDLPALKNIRKKNOLYDSTSELOHKEKAIOEONTMLAKRIKEKEKILR 180

Qy 180 GOOE--GOLVOCSSSVLLPQ 199  
Db 181 AOOEQWDOQONCHNMPPLPQ 202

#### RESULT 7

MADS box protein ap1 - white mustard

N:Alternate names: floral homeotic protein ap1

C:Species: Sinapis alba (white mustard)

C>Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 24-Sep-1999

C:Accession: S52236

R:Menzel, G.; Apel, K.; Melzer, S.

submitted to the EMBL Data Library, September 1994

A:Description: Isolation and sequencing of the mustard (Sinapis alba L.) ap1 cDNA.

A:Reference number: S52236

A:Accession: S52236

A:Molecule type: mRNA

A:Residues: 1-254 <MEN>

A:Cross-references: EMBL:X81480; NID:g609252; PIDN:CAA57233.1; PID:g609253

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho

C:Keywords: DNA binding; nucleus; transcription regulation

F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 53.9%; Score 656; DB 2; Length 254;  
Best Local Similarity 64.1%; Pred. No. 3.9e-36;  
Matches 127; Conservative 38; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MGRGVOLKRIENKINRQVTFSSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINRQVTFSSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60

Qy 61 SCMERILERYRYLYSDKOLVGRDVSQSEBNVLEHAKEVLEKKNRMFGEDLDSL 120  
Db 61 SCMERILEKERYRYFAEROLVSNFQSPANWLTLEYSKRLKARIELLQRNHRHVMGEDLDSM 120

Qy 121 SLKELOSLEHOLDAAIKSIRSRKNQAMFESTSALOKKKAODHNNLSLKIKEREKKTG 180  
Db 121 SKRELONLEOQDLPALKNIRKKNOLYDSTSELOHKEKAIOEONTMLAKRIKEKEKILR 180

Qy 181 OOEQOLVOCSSSVLLP 198  
Db 181 AOOEQWDOQONCHNMP 198

#### RESULT 8

MADS box protein homolog CAL - wild cabbage

C:Species: Brassica oleracea (wild cabbage)

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000

C:Accession: T14456

R:Kempin, S.A.; Savidge, B.; Yanofsky, M.F.

Science 267, 522-525, 1995

A:Title: Molecular basis of the cauliflower phenotype in Arabidopsis.

A:Reference number: Z18101; MUID:95125463; PMID:7824951

A:Accession: T14456

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-251 <KEM>

A:Cross-references: EMBL:L36926; NID:g642590; PIDN:AAA64790.1; PID:g642591

A:Experimental source: floral meristem

C:Genetics:

A:Gene: CAL

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho

C:Keywords: DNA binding; nucleus; transcription regulation

F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 51.0%; Score 621.5; DB 2; Length 251;  
Best Local Similarity 60.2%; Pred. No. 7e-34;  
Matches 121; Conservative 42; Mismatches 35; Indels 3; Gaps 2;

Qy 1 MGRGVOLKRIENKINRQVTFSSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60

Db	1	MGRGVEVKRIENKINRQVTEFSKRRAGLKKAHHSITLCAEVSILFESKGLTFEYSS	60
Oy	61	SCMEPIILERYDRYLXSDKOLVGRD--VSQENWVLEHAKLKARVEYLEKKRNFMG	118
Db	61	SCMEVLEHYERYSYAEOLKLPVDSHNAQTNNISVEYSRLKATIELLERORHYLG	120
Oy	119	SLSLKELOSLHODAAIKFSIRKNOAMFESIALQKKDAQODNNLSLKIKIREKK	178
Db	121	SISIKELQNLBQOLDPYSLKIHRSKKNQLMHESLNHQKKEKELLENSMLAQNIR	180
Oy	179	TGQGGOLVQCSNSSSVLLPQ	199
Db	181	LRTHONQSQ--QNRSHHVAEP	200

RESULT 9  
T03410  
MADS box protein - maize  
C:Species: Zea mays (maize)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 24-Sep-1999  
C:Accession: T03410  
R:Maia, M.; Mandel, M.A.; Lerner, D.R.; Yanofsky, M.F.; Schmidt, R.J.  
Plant J. 8, 845-854, 1995  
A:Title: A characterization of the MADS-box gene family in maize.  
A:Reference number: Z14928; MID:J6132144; PMID:8580958  
A:Accession: T03410  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-273 <MEN>  
A:Cross-references: EMBL:L64600; NID:g939784; PIDN:AAB00081.1; PID:g939785  
C:Genetics:  
A:Note: ZAP1  
C:Superfamily: transcription factor squa; serum response factor DNA-binding  
J:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

RESULT 10  
T14737  
MADS box protein - sorghum (fragment)  
C:Species: Sorghum bicolor (sorghum)  
C:Date: 20-Sep-1999 #sequence-revision 20-Sep-1999 #ext\_change 21-Jul-2000  
C:Accession: T14737  
R:Grego, R.; Stagi, L.; Colombo, L.; Angenent, G.C.; Sari-Gorla, M.; Pe, M.E.  
Mol. Gen. Genet. 255, 615-623, 1997  
A:Title: MADS box genes expressed in developing inflorescences of rice and sorghum  
A:Reference number: Z15292; PMID:97218034; PMID:9063695  
A:Accession: T14737  
A>Status: preliminary; translated from GB/EMBL/DBJ

```

A:Molecule type: mRNA
A:Residues: 1-228 <GRE>
A:Cross-references: EMBL:U032110; NID:g1905933; PID:AAB50181.1; PID:g1905934
C:Genetics:
A:Gene: MADS2
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain
C:Keywords: DNA binding; nucleus; transcription regulation

Query Match          47.2%; Score 575.5; DB 2; Length 228;
Best Local Similarity 51.9%; Pred. No. 6.5e-31;
Matches 120; Conservative 40; Mismatches 58; Indels 13; Gaps 3;

QY 5 RVOLRIENKIRKROYTFESKRSGSLTKKAHEISVLCDAEVALIVFSSKKRLFEYSDSCME 64
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 KVOLRIENKIRKROYTFESKRNGSLTKKAHEISVLCDAEAAVIVFSPKKLFEYATDSMD 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 RILLEYRYDLYSDKQVGRVDSQSENVWLEHAKLKARVEVLEKKNRNFNGEDLSLSKE 124
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 KILLERYERYSAEKALISAESESEGNWCHEVRKLAKIETIQCKHLMGDDLSLNPK 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 LOSLEHODDAKTSIRSKKNQAMFESISALOKKDALODHNHNSLLTIKEREKKTG---Q 181
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 LOOLEDOOLESSLKHSRKSHLMASIESIETQKKERSLOEBEKKALQKEIAERQKAAASROQ 180
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 QEGOLVQGSNNSSVLLPQYCVTSSRDGFVFNVGCGNGGASSLTPENSLLPA 232
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 QQGAVGPADDTGG---PDKLL-----IVLLHDEAGSAGSAASTKHMLPA 221
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 11  
T14457  
MADS box protein homolog CAL - broccoli1  
C.Species: Brassica oleracea var. botrytis (broccoli1)  
C.Date: 20-Sep-1999 #sequence.revision 20-Sep-1999 #text.change 21-Jul-2000  
C.Accession: T14457  
R.Kempin, S.A.; Savidge, B.; Yanofsky, M.F.  
Science 267, 522-525, 1995  
A.Title: Molecular basis of the cauliflower phenotype in Arabidopsis.  
A.Reference number: 218101; MUID:95125463; PMID:7824951  
A.Accession: T14457  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: mRNA  
A.Residues: 1-150 <KEM>  
A.Cross-references: EMBL:L36927; NID:g642592; PIDs:AAA64791.1; PID:g642593  
A.Experimental source: curd (inflorescence meristem)  
C.Genetics:  
A.Gene: CAL  
C.Superfamily: transcription factor squa; serum response factor DNA-binding domain ho  
C.Keywords: DNA binding; nucleus; transcription regulation

RESULT 12  
T10714  
MADS-box protein CMR1 - clove pink  
C:Species: Dianthus caryophyllus (clove pink)  
C:Date: 16-Jul-1999 #sequence-revision 16-Jul-1999 #text-change 21-Jan-2000  
#Accession: T10714

R.Baudinette, S.C.; Savin, R.W.  
submitted to the EMBL Data Library, March 1995  
A:Description: Carnation MADS box genes.  
A:Reference number: 217094  
A:Accession: T10714  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-233 <BAU>  
A:Cross-references: EMBL:L40404; NID:9695316; PID:9695317  
A:Experimental source: cv. Scania; petals  
C:Genetics:  
A:Gene: CM1  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C:Keywords: DNA binding; transcription factor; transcription regulation  
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 41.8%; Score 509; DB 2; Length 233;  
Best Local Similarity 44.3%; Pred. No. 1.5e-26;  
Matches 109; Conservative 45; Mismatches 68; Indels 24; Gaps 3;

OY 1 MGRGVOLKRIENKINROVTFSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Db 1 MGRGVEIKRIENKINROVTFKRRNGLLKKAHEISVLCDAEVALIVSSKGLFEFCST 60  
OY 61 SCMERILERYDRYLSDKOLVGRDVSSENNVLEHAKEIKARVEYLEKKNRMFGEDLDSL 120  
Db 61 SCMNKTLERYQRCYSGLSE-TSPSKTERESSYQVEYLKIKAVDVLDQRHNLGSDLEGL 119  
OY 121 SKELOSLERHOLDAIAKISRSKKNQAFESISALOKKKALADHNNLSLKIKERK-- 174  
Db 120 STEKLEOLEHOLDKSLRQIRSIKTOHMDLADLQKKEEMLFESNRALKTKEESCASF 179  
OY 175 -----REKKTQGEQOLVCCSSSVLLPQYCVITSSRQGFVERVGENGASSLTEPNSL 229  
Db 180 PNWDVROGDFEFLPPLPCNNNIQI-----GYNEATQDQNNATTSAQNVHGF 227  
OY 230 LPAMWL 235  
Db 228 AQGWML 233

## RESULT 13

T09569  
MADS box protein MADS1 - Monterey pine  
C:Species: Pinus radiata (Monterey pine)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jan-2000  
C:Accession: T09569  
R:Mouradov, A.; Glassick, T.; Vivian-Smith, A.; Teasdale, R.  
submitted to the EMBL Data Library, December 1995  
A:Reference number: 216739  
A:Accession: T09569  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-245 <MOD>  
A:Cross-references: EMBL:U42399; NID:g1206002; PID:g1206003  
C:Genetics:  
A:Gene: MADS1  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C:Keywords: DNA binding; transcription regulation  
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 41.1%; Score 500; DB 2; Length 245;  
Best Local Similarity 43.2%; Pred. No. 6.3e-26;  
Matches 108; Conservative 53; Mismatches 69; Indels 20; Gaps 5;

OY 1 MGRGVOLKRIENKINROVTFSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Db 1 MGRGVEIKRIENKINROVTFKRRNGLLKKAHEISVLCDAEVALIVSSKGLFEFCSS 60  
OY 61 SCMERILERYDRYLSDKOLVGRDVSSENNVLEHAKEIKARVEYLEKKNRMFGEDLDSL 120  
Db 61 SSMKTKTEKYKCSYGLSE-TNCSINEMONSQYDYLKKAHEISVLCDAEVALIVSSKGLFEGLPL 119

OY 121 SKELOSLERHOLDAIAKISRSKKNQAFESISALOKKKALADHNNLSLKIKERKKTG 180  
Db 120 NSEKLEOLEHOLDENSIKQIRSAKTQPMFQDLHLHLDKEQMLVEANRELKKEESNTRILP 179  
OY 181 QOEGOLVCCSSSV-LLPQYCVITSSRQGFVERVGG-----ENGASSLT-----E 225  
Db 180 LRLGWEAEDHNNISYRRLP-----TOSQGLFQPLGYPYPMQIGYNPAGSNELNVSPADQH 235  
OY 226 PMSLLPAMWL 235  
Db 236 PNGTIPGWML 245

## RESULT 14

S51935  
probable MADS-box protein dal1 - Norway spruce  
C:Species: Picea abies (Norway spruce)  
C:Date: 14-Jul-1995 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
C:Accession: T14846; S51935  
R:Randre, K.; Albert, V.A.; Sundas, A.; Engstroem, P.  
plant Mol. Biol. 27, 69-78, 1995  
A:Title: Conifer homologues to genes that control floral development in angiosperms.  
A:Reference number: S51934; MUID:95170009; PMID:7865797  
A:Accession: T14846  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-261 <TAN>  
A:Cross-references: EMBL:X80902; NID:9695685; PIDN:CAAS6864.1; PID:9695686  
A:Accession: S51935  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 92-156 <TA2>  
C:Genetics:  
A:Gene: dal1  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain ho  
C:Keywords: DNA binding; transcription regulation  
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 40.8%; Score 497.5; DB 2; Length 261;  
Best Local Similarity 51.3%; Pred. No. 9.9e-26;  
Matches 101; Conservative 45; Mismatches 42; Indels 9; Gaps 3;

OY 1 MGRGVOLKRIENKINROVTFSKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60  
Db 1 MGRGVEIKRIENKINROVTFKRRNGLLKKAHEISVLCDAEVALIVSTRKKTLEFSS 60  
OY 61 SCMERILERYDRYLSDKOLVGRDVSSENNVLEHAKEIKARVEYLEKKNRMFGEDLDSL 120  
Db 61 S-MNKTLEERYEKCSYAMQDTTGVSDREAQNMHWQEVTKLKGVELLQSRGHLGSDLEGL 119  
OY 121 SKELOSLERHOLDAIAKISRSKKNQAFESISALOKKKALADHNNLSLKIKERK-- 178  
Db 120 NVKLEOLEHOLDVALAHRSKRTQVMDQTELRQERLHEVKSLSLOKLSFTEGRDV 179  
OY 179 -TGQEGOLVCCSSSS 194  
Db 180 ITG-----IEQTSNNT 191

## RESULT 15

T09603  
MADS-box protein 3 - Monterey pine  
C:Species: Pinus radiata (Monterey pine)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jan-2000  
C:Accession: T09603  
R:Mouradov, A.; Loopsira, C.; Southerton, S.; Glassick, T.; Marshal, H.; Teasdale, R.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: 216765  
A:Accession: T09603  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-261 <MOD>  
A:Cross-references: EMBL:U76726; NID:g2160700; PID:g2160701



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 27, 2003, 12:34:37 ; Search time 33 Seconds  
(without alignments)  
1511.012 Million cell updates/sec

Title: US-09-981-087a-2

Perfect score: 1218  
Sequence: 1 MGRGVOLKRIENKINROVT.....LTPEPNSILPAMMLPPTTNE 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rviro:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	794	65.2	244	10 Q39401	039401 betula verr
2	772.5	63.4	245	10 Q9XHR7	09xhr7 nicotiana s
3	769.5	63.2	255	10 Q9ZRA5	09zra5 malus domes
4	761.5	62.5	247	10 Q9SEGT	09seg7 capsicum an
5	756.5	62.1	245	10 Q9SBO0	09sbo0 petunia hyb
6	753	61.8	246	10 Q9SBQ1	09sbq1 petunia hyb
7	751.5	61.7	245	10 Q9ZTY3	09zty3 nicotiana t
8	741	60.8	257	10 Q41356	041356 silene latl
9	735.5	60.4	244	10 Q9FUI3	09fui3 eucalyptus
10	732.5	60.1	245	10 Q9FUI8	09fui8 eucalyptus
11	703.5	57.8	205	10 Q9FUI2	09fui2 eucalyptus
12	695	57.1	252	10 Q94IM9	094im9 antirrhinum
13	683	56.1	239	10 Q82695	082695 malus domes
14	683	56.1	248	10 Q38742	038742 antirrhinum
15	680	55.8	240	10 Q9ARI3	09ari3 pisum sativ
16	676.5	55.5	245	10 Q9ATE2	09ate2 petunia hyb

17	676	55.5	242	10 Q9XHR8	09xhr8 nicotiana t
18	670	55.0	242	10 Q9ZTY2	09zty2 nicotiana t
19	669	54.9	260	10 Q39400	039400 betula verr
20	663	54.4	244	10 Q8S4L5	08s4l5 lycopersico
21	662	54.4	251	10 Q9SEGI	09seg1 arabidopsis
22	661	54.3	243	10 Q39399	039399 betula verr
23	659	54.1	254	10 Q9XEL0	09xel0 sinapis alb
24	656	53.9	242	10 Q9XHR6	09xhr6 nicotiana s
25	656	53.7	256	10 Q96355	096355 brassica ol
26	654	53.7	256	10 Q96356	096356 brassica ol
27	649	53.3	244	10 Q82128	082128 trifolium ae
28	648	53.2	248	10 Q8RVR0	08rvr0 hellianthus
29	648	53.2	256	10 Q39371	039371 brassica ol
30	638	52.4	254	10 Q9SRK9	09skr9 brassica ra
31	635	52.1	276	10 Q9LEI0	09lei0 hordeum vul
32	634.5	52.1	246	10 Q41355	041355 silene latl
33	629	51.6	245	10 Q9ZTY7	09zty7 lolium temu
34	629	51.6	247	10 Q9SNX1	09snx1 dendrobium
35	628	51.6	240	10 Q948U1	0948u1 magnolia pr
36	627	51.5	246	10 Q9MAV7	09may7 oryza sativ
37	627	51.5	255	10 Q39081	039081 arabidopsis
38	623	51.1	221	10 Q9ZS25	09zst5 gerbera hyb
39	621.5	51.0	251	10 Q39375	039375 brassica ol
40	621	51.0	246	10 Q9SEX0	09sex0 oryza sativ
41	620.5	50.9	261	10 Q9ZTY6	09zty6 lolium temu
42	618	50.7	246	10 Q9M7C6	09m7c6 oryza sativ
43	611	50.2	244	10 Q9LEI2	09lei2 hordeum vul
44	610.5	50.1	273	10 Q41829	041829 zea mays (m
45	607.5	49.9	249	10 Q9SMB3	09smb3 oryza sativ

## ALIGNMENTS

## RESULT 1

Q39401 ID Q39401 PRELIMINARY; PRT: 244 AA.  
AC Q39401:  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE MADS5 protein.  
OS MADS5.  
GN Betula verrucosa (White birch) (Betula pendula).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fagales; Betulaceae; Betula.  
OX NCBI\_TaxID=3505;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=FEMALE INFLORESCENCE;  
RA Elo A., Lemmetyinen J., Tuunen M.L., Tikka L., Sopanen T.;  
RT "Three MADS box genes homologous to SOUMOSA and APERAL have  
RT different expression patterns in silver birch (Betula pendula  
RT Roth.).";  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
CC -i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -i- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.  
CC EMBL: X99655; CAA67969.1; -.  
CC HSSP: P11746; IMNM.  
DR TRANSFAC: T03048; -.  
DR InterPro: IPR002487; TF\_Kbox.  
DR InterPro: IPR002100; TF\_MADSbox.  
DR Pfam: PF01486; K-box; 1.  
DR Pfam: PF00319; SRF-TF; 1.  
DR PRINTS: PR00404; MADSDOMAIN.  
DR SMART: SM00432; MADS: 1.  
DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
DR PROSITE: PS50066; MADS\_BOX\_2; 1.  
KW DNA-binding; Nuclear protein; Transcription regulation.  
SQ SEQUENCE 244 AA; 28174 MW; 358FD25D084ECAB4 CRC64;

Query Match 65.2% Score 794; DB 10; Length 244;

Best Local Similarity 68.5%; Pred. No. 1.2e-44;  
Matches 165; Conservative 28; Mismatches 42; Indels 6; Gaps 3;

QY 1 MGRGVOLKRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60

QY 61 SCMERILEYRDYLSKQVGRDVSQSENVYLEHAKLAKARVEVLEKKRNFMGEDIDL 120  
Db 61 SCMERILEYERYSTYERQQLANDNESTGWTLEHAKLAKARVEVLEKKRNFMGEDIDL 120

QY 121 SKELOSLEHODAAIKSTRSRKNQAMFESISALOKKDALODHNNLSLKKIKEREKKTG 180  
Db 121 SKELOSLEHODAAIKSTRSRKNQAMFESISALOKKDALODHNNLSLKKIKEREKKTG 180

QY 181 QOQOEQOQSHLTDVSPSLPQPLQSSSLNIGSSQOARG-NORVDEGTPPHRANMLLPWML 239  
Db 181 QOQOEQOQSHLTDVSPSLPQPLQSSSLNIGSSQOARG-NORVDEGTPPHRANMLLPWML 239

QY 236 R 236  
Db 240 R 240

RESULT 2  
Q9XHR7 PRELIMINARY: PRT: 245 AA.  
AC Q9XHR7;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE MADS-box protein MADS1.  
GN NSMADS1.  
OS Nicotiana sylvestris (Wood tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4096;  
RN [1]  
RA Jang S., An G.;  
RT "NEMADS1, a member of the MADS gene family from Nicotiana sylvestris";  
RL J. Plant Biol. 42:85-87(1999).  
DR EMBL: AF068725; AAD39056.1; -;  
DR HSSP: P11746; 1MNM.  
DR InterPro: IPR002487; TF\_Kbox.  
DR InterPro: IPR002100; TF\_MADSbox.  
DR Pfam: PF01486; K-box. 1.  
DR Pfam: PF00319; SRP-TF. 1.  
DR PRINTS: PR00404; MADSDOMAIN.  
DR SMART: SM00432; MADS. 1.  
DR PROSITE: PS50066; MADS\_BOX\_2. 1.  
SQ SEQUENCE 245 AA: 28297 MW; 234D53DA0D606450 CRC64;

Query Match 63.4%; Score 772.5; DB 10; Length 245;  
Best Local Similarity 66.5%; Pred. No. 3e-43;  
Matches 161; Conservative 30; Mismatches 44; Indels 7; Gaps 3;

QY 1 MGRGVOLKRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60

QY 61 SCMERILEYRDYLSKQVGRDVSQSENVYLEHAKLAKARVEVLEKKRNFMGEDIDL 120  
Db 61 SCMERILEYERYSTYERQQLANDNESTGWTLEHAKLAKARVEVLEKKRNFMGEDIDL 120

QY 121 SKELOSLEHODAAIKSTRSRKNQAMFESISALOKKDALODHNNLSLKKIKEREKKTG 180  
Db 121 SKELOSLEHODAAIKSTRSRKNQAMFESISALOKKDALODHNNLSLKKIKEREKKTG 180

QY 181 QOQOEQOQSHLTDVSPSLPQPLQSSSLNIGSSQOARG-NORVDEGTPPHRANMLLPWML 239  
Db 181 QOQOEQOQSHLTDVSPSLPQPLQSSSLNIGSSQOARG-NORVDEGTPPHRANMLLPWML 239

Db 181 QOQOEQOQSHLTDVSPSLPQPLQSSSLNIGSSQOARG-NORVDEGTPPHRANMLLPWML 239  
QY 235 LR 236  
Db 240 LR 241

RESULT 3  
Q9ZRA5 PRELIMINARY: PRT: 255 AA.  
AC Q9ZRA5;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE MADS-box protein 2.  
OS Malus domestica (Apple) (Malus sylvestris).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroids I; Rosales; Rosaceae; Maloideae; Malus.  
OX NCBI\_TaxID=3750;  
RN [1]  
RA SEQUENCE FROM N.A.  
RC STRAIN=CY. FUJI; TISSUE=FLOWER BUDS;  
RX MEDLINE=99373384; PubMed=10444080;  
RA Sung S.K., Yu G.H., An G.;  
RT "Characterization of MdMADS2, a member of the SQUAMOSA subfamily of genes, in apple";  
RL Plant Physiol. 120:969-978(1999).  
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.  
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.  
DR EMBL: U78948; AAC83170.1; -;  
DR HSSP: P11746; 1MNM.  
DR TRANSFAC: T04707; -;  
DR InterPro: IPR002487; TF\_Kbox.  
DR InterPro: IPR002100; TF\_MADSbox.  
DR Pfam: PF01486; K-box. 1.  
DR Pfam: PF00319; SRP-TF. 1.  
DR PRINTS: PR00404; MADSDOMAIN.  
DR SMART: SM00432; MADS. 1.  
DR PROSITE: PS00350; MADS\_BOX\_1. 1.  
DR PROSITE: PS50066; MADS\_BOX\_2. 1.  
KW DNA-binding; Nuclear protein; Transcription regulation.  
SQ SEQUENCE 255 AA: 29492 MW; DA34B2FE6430203 CRC64;

Query Match 63.2%; Score 769.5; DB 10; Length 255;  
Best Local Similarity 63.5%; Pred. No. 5e-43;  
Matches 162; Conservative 28; Mismatches 42; Indels 23; Gaps 4;

QY 1 MGRGVOLKRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60

QY 61 SCMERILEYRDYLSKQVGRDVSQSENVYLEHAKLAKARVEVLEKKRNFMGEDIDL 120  
Db 61 SCMERILEYERYSTYERQQLANDNESTGWTLEHAKLAKARVEVLEKKRNFMGEDIDL 120

QY 121 SKELOSLEHODAAIKSTRSRKNQAMFESISALOKKDALODHNNLSLKKIKEREKKTG 180  
Db 121 SKELOSLEHODAAIKSTRSRKNQAMFESISALOKKDALODHNNLSLKKIKEREKKTG 180

QY 181 QOQOEQOQSHLTDVSPSLPQPLQSSSLNIGSSQOARG-NORVDEGTPPHRANMLLPWML 239  
Db 181 QOQOEQOQSHLTDVSPSLPQPLQSSSLNIGSSQOARG-NORVDEGTPPHRANMLLPWML 239

RESULT 4  
Q9SEG7 PRELIMINARY: PRT: 247 AA.  
AC Q9SEG7;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE MADS-box protein 2.  
OS Malus domestica (Apple) (Malus sylvestris).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroids I; Rosales; Rosaceae; Maloideae; Malus.  
OX NCBI\_TaxID=3750;  
RN [1]  
RA SEQUENCE FROM N.A.  
RC STRAIN=CY. FUJI; TISSUE=FLOWER BUDS;  
RX MEDLINE=99373384; PubMed=10444080;  
RA Sung S.K., Yu G.H., An G.;  
RT "Characterization of MdMADS2, a member of the SQUAMOSA subfamily of genes, in apple";  
RL Plant Physiol. 120:969-978(1999).  
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.  
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.  
DR EMBL: U78948; AAC83170.1; -;  
DR HSSP: P11746; 1MNM.  
DR TRANSFAC: T04707; -;  
DR InterPro: IPR002487; TF\_Kbox.  
DR InterPro: IPR002100; TF\_MADSbox.  
DR Pfam: PF01486; K-box. 1.  
DR Pfam: PF00319; SRP-TF. 1.  
DR PRINTS: PR00404; MADSDOMAIN.  
DR SMART: SM00432; MADS. 1.  
DR PROSITE: PS00350; MADS\_BOX\_1. 1.  
DR PROSITE: PS50066; MADS\_BOX\_2. 1.  
KW DNA-binding; Nuclear protein; Transcription regulation.  
SQ SEQUENCE 255 AA: 29492 MW; DA34B2FE6430203 CRC64;

Query Match 63.2%; Score 769.5; DB 10; Length 255;  
Best Local Similarity 63.5%; Pred. No. 5e-43;  
Matches 162; Conservative 28; Mismatches 42; Indels 23; Gaps 4;

QY 1 MGRGVOLKRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
Db 1 MGRGVOLKRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60

QY 61 SCMERILEYRDYLSKQVGRDVSQSENVYLEHAKLAKARVEVLEKKRNFMGEDIDL 120  
Db 61 SCMERILEYERYSTYERQQLANDNESTGWTLEHAKLAKARVEVLEKKRNFMGEDIDL 120

QY 121 SKELOSLEHODAAIKSTRSRKNQAMFESISALOKKDALODHNNLSLKKIKEREKKTG 180  
Db 121 SKELOSLEHODAAIKSTRSRKNQAMFESISALOKKDALODHNNLSLKKIKEREKKTG 180

QY 181 QOQOEQOQSHLTDVSPSLPQPLQSSSLNIGSSQOARG-NORVDEGTPPHRANMLLPWML 239  
Db 181 QOQOEQOQSHLTDVSPSLPQPLQSSSLNIGSSQOARG-NORVDEGTPPHRANMLLPWML 239



DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE MADS box protein.  
 GN MADS6.  
 OS Capsicum annuum (Bell pepper).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.  
 OX NCBI\_TaxID=4072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21351847; PubMed=11459226;  
 RA Sung S.-K., Moon Y.-H., Chung J.-E., Lee S.-Y., Park H.-G., An G.;  
 RT "Characterization of MADS box genes from hot pepper."  
 RL Mol. Cells 11:352-359(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Jung J.-Y., Moon Y.-H., Chung J.-E., Sung S.-K., An G.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)  
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.  
 DR EMBL; AF130118; AAF22139.2; -.  
 DR HSSP; P11746; 1NMN.  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRF-TE; 1.  
 DR PRINTS; PR00404; MADSDOMAIN.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE; PS00066; MADS\_BOX\_2; 1.  
 KW DNA-binding; Nuclear protein; Transcription regulation.  
 SQ SEQUENCE 247 AA; 28669 MW; C44714D6E8627C1 CRC64;

Query Match 62.5%; Score 761.5; DB 10; Length 247;  
 Best Local Similarity 66.4%; Pred. No. 1.6e-42;  
 Matches 162; Conservative 30; Mismatches 43; Indels 9; Gaps 4;

OY 1 MGRGVQLKRIENKINROVTFKRRSGLLKKAHEISVLCDAVALIVSSKGLFEYSTD 60  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 1 MGRGVQLKRIENKINROVTFKRRSGLLKKAHEISVLCDAVALIVSSKGLFEYSTD 60  
 OY 61 SCMERILERYDRYLXSDKOLVGRDVSSENNVLEHAKLKARVEYLEKKRNFMGEDLST 120  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 61 SCMERILERYDRYLXSDKOLVGRDVSSENNVLEHAKLKARVEYLEKKRNFMGEDLST 120  
 OY 121 SLKELQSLHOLDAAIKSIRSRKNOAFESISALQKKDALKADHNNLSLKIKEREKKTG 180  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 121 SKKEIQNLQQLDSALKHRSRKNQLMHESISLQKKDALKQDQNNLSKQMKEREKOLA 180  
 OY 181 QO---EQLVQCSNSSSVLPQYCVTSRSGFVERVGENG---GASSLTEPN-SLPA 232  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 181 QOHTPEWQNDHDLNLSSEFGLP-HPFNNHLEGVYPRAGDNGEVBSSRQOQNAVMP 239  
 OY 233 WMLR 236  
 |||||  
 DB 240 WMLR 243  
 RESULT 5  
 O9SBQ0 PRELIMINARY; PRT; 245 AA.  
 AC O9SBQ0.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Floral binding protein 26.  
 OS Petunia hybrida (Petunia).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
 OX NCBI\_TaxID=4102;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. M115;  
 RX MEDLINE=20002442; PubMed=10529428;  
 RA Immink R.G.H., Hannapel D.J., Ferrario S., Busscher M., Franken J.,  
 RA Lookeren Campagne M.M., Angenent G.C.;  
 RT "A petunia MADS box gene involved in the transition from vegetative to  
 RT reproductive development."  
 RL Development 126:5117-5126(1999).  
 DR EMBL; AF16783; AAF19164.1; -.  
 DR HSSP; P11746; 1NMN.  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRF-TE; 1.  
 DR PRINTS; PR00404; MADSDOMAIN.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00066; MADS\_BOX\_2; 1.  
 SQ SEQUENCE 245 AA; 28161 MW; 1D5913E2D1DBE49E CRC64;

Query Match 62.1%; Score 756.5; DB 10; Length 245;  
 Best Local Similarity 66.1%; Pred. No. 3.4e-42;  
 Matches 160; Conservative 29; Mismatches 46; Indels 7; Gaps 4;

OY 1 MGRGVQLKRIENKINROVTFKRRSGLLKKAHEISVLCDAVALIVSSKGLFEYSTD 60  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 1 MGRGVQLKRIENKINROVTFKRRSGLLKKAHEISVLCDAVALIVSSKGLFEYSTD 60  
 OY 61 SCMERILERYDRYLXSDKOLVGRDVSSENNVLEHAKLKARVEYLEKKRNFMGEDLST 119  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 61 SCMERILERYDRYLXSDKOLVGRDVSSENNVLEHAKLKARVEYLEKKRNFMGEDLST 120  
 OY 120 ISLKLQSLHOLDAAIKSIRSRKNOAFESISALQKKDALKADHNNLSLKIKEREKKT 179  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 121 LSKELQNLQQLDSALKHRSRKNQLMHESISLQKKDALKQDQNNLSKQMKEREKEL 180  
 OY 180 GQOEQLVQCS--NSSSVLPQYCVTSRSGFVERVGENG---GASSLTEPN-SLPA 234  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 181 AQQSQEPQSHDNLNSSFVLSQ-PLNSLHLEGAIFYPSAGDNGEVBSSRQPPNTVPM 239  
 OY 235 LR 236  
 |||||  
 DB 240 LR 241  
 RESULT 6  
 O9SBQ1 PRELIMINARY; PRT; 246 AA.  
 AC O9SBQ1.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE MADS box transcription factor.  
 GN PFG.  
 OS Petunia hybrida (Petunia).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
 OX NCBI\_TaxID=4102;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. M115;  
 RX MEDLINE=20002442; PubMed=10529428;  
 RA Immink R.G.H., Hannapel D.J., Ferrario S., Busscher M., Franken J.,  
 RA Lookeren Campagne M.M., Angenent G.C.;  
 RT "A petunia MADS box gene involved in the transition from vegetative to  
 RT reproductive development."  
 RL Development 126:5117-5126(1999).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.  
 DR EMBL; AF16782; AAF19721.1; -.  
 DR HSSP; P11746; 1NMN.  
 DR InterPro; IPR002487; TF\_Kbox.

DR InterPro: IPR002100; TF\_MADSbox.  
 DR Pfam: PF01486; K-box; 1.  
 DR Pfam: PF00319; SRF-TF; 1.  
 DR PRINTS: PR00404; MADSMAIN.  
 DR SMART: SM00432; MADS; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE: PS50066; MADS\_BOX\_2; 1.  
 DR DNA-binding: Nuclear protein; Transcription regulation.  
 SO SEQUENCE 246 AA; 28539 MW; C8713413ACD5DA6B CRC64;

Query Match 61.8%; Score 753; DB 10; Length 246;  
 Best Local Similarity 63.1%; Pred. No. 5.7e-42;

Matches 157; Conservative 34; Mismatches 38; Indels 20; Gaps 4;

OY 1 MGRGRVQLRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
 DB 1 MGRGRVQLRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
 OY 61 SCMERLEERYDRLYSDKOLVGRDVSOSENVYLEHAKLKARVEYLEKKNRMGEDDLSL 120  
 DB 61 SCMERLEERYERYSVAROLVSTFDSHSSPGSMNLEHAKLKARIEVVOHNGMGEDDLSL 120  
 OY 121 SLKELOSLERHOLDAAIKTSIRSRKNQAMFESISALOKKDALODNNNSLLKIKEREKKTG 180  
 DB 121 SKMDLQNLHQQLDLSLKHRSRKNQMLHESISLQKKDSDLODNNLSLKKVREKELA 180  
 OY 181 Q-----EGOLVQCSNSSSVLLPQ-----YCVTSRSDGFERYGNGGASSTLEPN 227  
 DB 181 QOTQWEOQNHNHINSSSVLLPQPLDSPHLEAYYSTVD-----NGEVEGASQ-QQPA 233  
 OY 228 SLPLPAMLR 236  
 DB 234 NTMPFWMRLR 242

## RESULT 7

O9ZTV3 PRELIMINARY; PRT; 245 AA.

AC O9ZTV3;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE MAP1-1.  
 GN MAP1-1.  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxId=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=XANTHI;  
 RA Wu Y.H., Li O., Zhang J.-S., Li Y.;  
 RL Submitted (JUN-1997) to the EMBL/Genbank/DBD databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.  
 DR EMBL: AF009126; AAD01421.1; -  
 DR HSSP: P11746; 1MMN.  
 DR InterPro: IPR002487; TF\_Kbox.  
 DR InterPro: IPR002100; TF\_MADSbox.  
 DR Pfam: PF01486; K-box; 1.  
 DR Pfam: PF00319; SRF-TF; 1.  
 DR PRINTS: PR00404; MADSMAIN.  
 DR SMART: SM00432; MADS; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE: PS50066; MADS\_BOX\_2; 1.  
 DR DNA-binding: Nuclear protein; Transcription regulation.  
 SO SEQUENCE 245 AA; 28223 MW; B696BCFCIAFB244C CRC64;

Query Match 61.7%; Score 751.5; DB 10; Length 245;  
 Best Local Similarity 64.9%; Pred. No. 7.1e-42;  
 Matches 157; Conservative 31; Mismatches 47; Indels 7; Gaps 3;

OY 1 MGRGRVQLRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
 DB 1 MGRGRVQLRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
 OY 61 SCMERLEERYDRLYSDKOLVGRDVSOSENVYLEHAKLKARVEYLEKKNRMGEDDLSL 120  
 DB 61 SCMERLEERYERYSVAROLVSTFDSHSSPGSMNLEHAKLKARIEVVOHNGMGEDDLSL 120  
 OY 121 SLKELOSLERHOLDAAIKTSIRSRKNQAMFESISALOKKDALODNNNSLLKIKEREKKTG 180  
 DB 121 CMELQNLHQQLDLSLKHRSRKNQMLHESISLQKKDSDLODNNLSLKKVREKELA 180  
 OY 181 QO---EGOLVQCSNSSSVLLPQYCVTSRSDGFERYGNGG--GASSTLEPNSLPAMM 234  
 DB 181 QOTQWEOQSHDLNLSVFLVQ-PLSSLHLEAYPTAGNGELEGGSRQOQONTVPMM 239  
 OY 235 LR 236  
 DB 240 LR 241

## RESULT 8

O41356 PRELIMINARY; PRT; 257 AA.

AC O41356;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE SLMS protein.  
 GN SLMS.  
 OS Silene latifolia (White campion).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxId=37657;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=INFLORESCENCE MERISTEMS AND DEVELOPING FLOWERS;  
 RX MEDLINE=95170282; PubMed=7866023;  
 RA Hardenack S., Ye D., Saedler H., Grant S.;  
 RT "Comparison of MADS-box gene expression in developing male and female  
 flowers of the dioecious plant white campion.";  
 RL Plant Cell 6:1775-1787(1994).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.  
 DR EMBL: X80492; CAA56659.1; -  
 DR HSSP: P11746; 1MMN.  
 DR TRANSFAC: T03177; -  
 DR InterPro: IPR002487; TF\_Kbox.  
 DR InterPro: IPR002100; TF\_MADSbox.  
 DR Pfam: PF01486; K-box; 1.  
 DR Pfam: PF00319; SRF-TF; 1.  
 DR PRINTS: PR00404; MADSMAIN.  
 DR SMART: SM00432; MADS; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE: PS50066; MADS\_BOX\_2; 1.  
 DR DNA-binding: Nuclear protein; Transcription regulation.  
 SO SEQUENCE 257 AA; 29815 MW; C8D1A1697AD9DEER CRC64;

Query Match 60.8%; Score 741; DB 10; Length 257;  
 Best Local Similarity 59.8%; Pred. No. 3.7e-41;  
 Matches 150; Conservative 37; Mismatches 48; Indels 16; Gaps 3;

OY 1 MGRGRVQLRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
 DB 1 MGRGRVQLRIENKINROVTFKRRSGLLKKAHEISVLCDAEVALIVFSSKGLFEYSTD 60  
 OY 61 SCMERLEERYDRLYSDKOLVGRDVSOSENVYLEHAKLKARVEYLEKKNRMGEDDLSL 120  
 DB 61 SCMERLEERYERYSVAROLVSTFDSHSSPGSMNLEHAKLKARIEVVOHNGMGEDDLSL 120  
 OY 121 SLKELOSLERHOLDAAIKTSIRSRKNQAMFESISALOKKDALODNNNSLLKIKEREKKTG 178  
 DB 121 SKMDLQNLHQQLDLSLKHRSRKNQMLHESISLQKKDSDLODNNLSLKKVREKELA 180

```
Db 121 SKELEONEHOLDTALKHTRSKNOIMFESIHLOKDKALOEHNNITLKKVKEKEKE 180
Oy 179 -----TQOGGOLVOCSSNS-----SSVLLPOYCVTSSND---GFEYRGGENGASSLT 224
Db 181 KEKATADDOAOAWOONQOELNPSAFFSSOVLPALNTRGNTEGSSVIVNEVAOTQNRSSS 240
Oy 225 EPNSSLPAWML 235
Db 241 NNNSLVPSMWL 251

RESULT 9
O9FU13
ID O9FU13 PRELIMINARY: PRT: 244 AA.
AC O9FU13:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE MADS-box protein EAP1.
OS Eucalyptus globulus (Blue gum).
OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Myrtaceae; Eucalyptus.
Ox NCBI_TaxID=34317;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98009992; PubMed=9349279;
RA Kyozuoka J., Harcourt R., Peacock W.J., Dennis E.S.;
RT "Eucalyptus has functional equivalents of the Arabidopsis Ap1 gene.";
RL Plant Mol. Biol. 35:573-584(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Kyozuoka J., Harcourt R., Peacock W.J., Dennis E.S.;
RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF305076; AAC24909.1; -.
DR HSSP; P11746; IMNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 244 AA; 28240 MW; 57AB7102DC01D5B9 CRC64;

Query Match 60.4%; Score 735.5; DB 10; Length 244;
Best Local Similarity 64.4%; Pred. No. 7.9e-41;
Matches 154; Conservative 34; Mismatches 44; Indels 7; Gaps 5;

Oy 1 MGRGVOLKRIENKINROYTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
Db 1 MGRGLQIKRIENKINROTTFESKRRAGLLKKAHEISVLCDAEVALIVSAKAKLEFYSTD 60
Oy 61 SCMERILERYDYLYXSDKOLVGRDVSQSENNWLEHAUKAKARVEYLEKKNRNMGEDLSTL 120
Db 61 SCMERILERYERYSYAEHOVLASFEISIGSWTLEHAUKAKARLEVLHRRNVRHFMGEDLSTL 120
Oy 121 SKELOSLEHODALAIKTSIRSRKNOAFESISALOKKDKALODHNNLSLTKIKEREKKTG 180
Db 121 SKELOLEHODALAIKTSIRSRKNOIMFESISALOKKDKALODHNNLSLTKIKEREKALA 180
Oy 181 OQEGOLVOCSSNS--SSVLLPOYCVTSSRDG-FVEYRGGENGASSLTPEP--NSLIPAWM 234
Db 181 OQ-AQWEGODHALDSPVVLPHYLPISLDINGSYQARHNGHDDG-ENLTQPRAGTLLPWT 237

RESULT 10
O9FUH8
ID O9FUH8 PRELIMINARY: PRT: 245 AA.
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AC O9FUH8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE MADS box protein Ap2L.
OS Eucalyptus globulus (Blue gum).
OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Myrtaceae; Eucalyptus.
Ox NCBI_TaxID=34317;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98009992; PubMed=9349279;
RA Kyozuoka J., Harcourt R., Peacock W.J., Dennis E.S.;
RT "Eucalyptus has functional equivalents of the Arabidopsis Ap1 gene.";
RL Plant Mol. Biol. 35:573-584(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Kyozuoka J., Harcourt R., Peacock W.J., Dennis E.S.;
RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF306349; AAC30923.1; -.
DR HSSP; P11746; IMNM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00319; SRP-TE; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 245 AA; 27991 MW; C081603C9A9AB6C CRC64;

Query Match 60.1%; Score 732.5; DB 10; Length 245;
Best Local Similarity 63.4%; Pred. No. 1.2e-40;
Matches 156; Conservative 27; Mismatches 46; Indels 17; Gaps 4;

Oy 1 MGRGVOLKRIENKINROYTFESKRRSGLLKKAHEISVLCDAEVALIVSSKGLFEYSTD 60
Db 1 MGRGVOLKRIENKINROYTFESKRRGGLKKAHEISVLCDAEVALIVSTKGLFEYATD 60
Oy 61 SCMERILERYDYLYXSDKOLVGRDVSQSENNWLEHAUKAKARVEYLEKKNRNMGEDLSTL 120
Db 61 CCMERILERYERYSYAESQVLTNNAETNGNWLEHAUKAKARLEILLQKNOKNLMGEEDLSTL 120
Oy 121 SKELOSLEHODALAIKTSIRSRKNOAFESISALOKKDKALODHNNLSLTKIKEREKKTG 180
Db 121 SKELOLEHODTALKHTRSKNOIMFESISALOKKDKALODHNNLSLTKIKEREKALA 180
Oy 181 OQEGOLVOCSSN-----SSVLLPOYCVTSSRDGFVEYRGGENGASSLTPEP--SL 229
Db 181 OQ-----TQWMDNQDDGLTSSSVILSQSLQPLNIGGPFYHPSGIEGAA--LGPQRRNMTL 234
Oy 230 LPAMWL 235
Db 235 FPSMWL 240

RESULT 11
O9FU12
ID O9FU12 PRELIMINARY: PRT: 205 AA.
AC O9FU12:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE MADS-box protein EAP2S.
OS Eucalyptus globulus (Blue gum).
OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Myrtaceae; Eucalyptus.
Ox NCBI_TaxID=34317;
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RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=98009992; PubMed=9349279;
Rt Kyocuka J., Harcourt R., Peacock W.J., Dennis E.S.;
Rt "Eucalyptus has functional equivalents of the Arabidopsis AP1 gene.";
Rt Plant Mol. Biol. 35:573-584(1997).
RN [2]
RX SEQUENCE FROM N.A.
RA Kyocuka J., Harcourt R., Peacock W.J., Dennis E.S.;
Rt Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AF030596; AAC27459.1; -
DR HSSP: P11746; 1MNM.
DR InterPro: IPR002487; TF_Kbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
SQ SEQUENCE 205 AA; 23690 MW; 2B1A305864269461 CRC64;

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Query Match 57.8%; Score 703.5; DB 10; Length 205;
Best Local Similarity 69.8%; Pred. No. 8e-39;
Matches 143; Conservative 23; Mismatches 28; Indels 11; Gaps 2;

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OY 1 MGRGRVQLKRIENKINROVTFESKRRSGGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
DB 1 MGRGRVQLKRIENKINROVTFESKRRSGGLLKAHEISVLCDAEVALIVFSTKGLFEYATD 60
OY 61 SCMERILERDYRLYSKQLVGRDVSQSENWVLEHAKLKAAREVLEKKNRNGEDLDL 120
DB 61 CCMERILERERYEYVAEQVLTNNAEKNGWTELEHAKLKAAREVLEKKNRNGEDLDL 120
OY 121 SKELOSLEHOLDAAIKSIRSKRNQAMFESISALQCKDKALDQHNNSLKKIKEREKKTG 180
DB 121 SKELOSLEHOLDAAIKSIRSKRNQAMFESISALQCKDKALDQHNNSLKKIKEREKKTG 180
OY 181 QOEGQLVOCNS-----SSSVLLP 198
DB 181 QO-----TQWDNPDQDGLTSSSGSLP 201

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RESULT 12
O941M9 PRELIMINARY: PRT: 252 AA.
AC O941M9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MADS-box transcription factor DEFH28.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21580397; PubMed=11722760;
RA Mueller B.M., Saedler H., Zachgo S.;
Rt "The MADS-box gene DEFH28 from Antirrhinum is involved in the
Rt regulation of floral meristem identity and fruit development.";
Rt Plant J. 28:169-180(2001).
DR EMBL: AY040247; AAK72467.1; -
DR InterPro: IPR002487; TF_Kbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PROSITE: PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE: PS50066; MADS_BOX_2; 1.

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SQ SEQUENCE 252 AA; 29293 MW; 20F75CB473836104 CRC64;
Query Match 57.1%; Score 695; DB 10; Length 252;
Best Local Similarity 59.0%; Pred. No. 3.6e-38;
Matches 147; Conservative 37; Mismatches 51; Indels 14; Gaps 4;

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OY 1 MGRGRVQLKRIENKINROVTFESKRRSGGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
DB 1 MGRGRVQLKRIENKINROVTFESKRRSGGLLKAHEISVLCDAEVALIVFSTKGLFEYSTE 60
OY 61 SCMERILERDYRLYSKQLVGRDVSQSENWVLEHAKLKAAREVLEKKNRNGEDLDL 120
DB 61 CCMERILERERYEYVAEQVLTNNAEKNGWTELEHAKLKAAREVLEKKNRNGEDLDL 120
OY 121 SKELOSLEHOLDAAIKSIRSKRNQAMFESISALQCKDKALDQHNNSLKKIKEREKKTG 180
DB 121 SMRELOSLEHOLDAAIKSIRSKRNQAMFESISALQCKDKALDQHNNSLKKIKEREKKTG 180
OY 181 QOEGQLVOCNS-----SSSVLLP 198
DB 181 QOEGQLVOCNS-----SSSVLLP 198
OY 228 SLTPAMWLR 236
DB 240 SLTPAMWLR 248

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RESULT 13
O82695 PRELIMINARY: PRT: 239 AA.
AC O82695;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MADS-box protein.
GN MADS.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. GRANNY SMITH;
RA Yao J.L., Dong Y.H., Kvarnheden A., Morris B.A.M.;
Rt "Seven MADS-box genes in apple are expressed in different parts of the
Rt fruit.";
Rt J. Am. Soc. Hortic. Sci. 124:8-13(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AJ000759; CAA04321.1; -
DR HSSP: P11746; 1MNM.
DR InterPro: IPR002487; TF_Kbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
SQ SEQUENCE 239 AA; 27983 MW; D2FC7FA5EBC9F5 CRC64;

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Query Match 56.1%; Score 683; DB 10; Length 239;
Best Local Similarity 67.8%; Pred. No. 2.1e-37;
Matches 135; Conservative 28; Mismatches 36; Indels 0; Gaps 0;

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OY 1 MGRGRVQLKRIENKINROVTFESKRRSGGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
DB 1 MGRGRVQLKRIENKINROVTFESKRRSGGLLKAHEISVLCDAEVALIVFSSKGLFEYATD 60
OY 61 SCMERILERDYRLYSKQLVGRDVSQSENWVLEHAKLKAAREVLEKKNRNGEDLDL 120
DB 61 CCMERILERERYEYVAEQVLTNNAEKNGWTELEHAKLKAAREVLEKKNRNGEDLDL 120

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ID	Q9AR13	PRELIMINARY;	PRT;	240 AA.
Db	61	SCMEDIIILEKYEKSYAEARQVLEPDEPESQGNWTFEESRLKAKAEVLQRRNRHITLGEDLDST	120	
QY	121	SLKEIQLSLEHOLDAIKSIRSRKKNQAMFESISALQKDKALODHNNSLLKTIKEREKKTG	180	
Db	121	TLKEITQNEEQDLDTALFKOIRLKNQLMNESISELQRRKRAIGENNLLAKKTIKEREKAA	180	
QY	181	QOEGQLVCCSNSSVLLPQ	199	
Db	181	QPOVNMEDQNHGIDLPLQ	199	
RESULT 14				
ID	Q38742	PRELIMINARY;	PRT;	248 AA.
AC	Q38742;			
DT	01-NOV-1996 (Tremblrel. 01, Created)			
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)			
DT	01-MAR-2002 (Tremblrel. 20, Last annotation update)			
DE	SQUA.			
GN	SQUAMOSA.			
OS	Antirrhinum majus (Garden snapdragon).			
OC	Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;			
CC	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;			
OX	Asteridae; easterids I; Iamiales; Veroniceae; Antirrhinum.			
NCBI_TaxID	4151;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-T53;			
RX	MEDLINE-92224862; PubMed-1563342;			
RA	Huijser P., Klein J., Lonnig W.E., Meijer H., Saedler H., Sommer H.;			
RT	"Bracteomania, an inflorescence anomaly, is caused by the loss of			
RL	function of the MADS-box gene squamosa in Antirrhinum majus.";			
CC	EMBO J. 11:1239-1249(1992).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.			
DR	EMBL; X51701; CAA45228.1; -.			
DR	HSSP; P11746; 1MM.			
DR	TRANSFAC; T03178; -.			
DR	InterPro; IPR002487; TF_KDox.			
DR	InterPro; IPR002100; TF_MADSbox.			
DR	Pfam; PF01486; K-box; 1.			
DR	Pfam; PF00319; SRF-TE; 1.			
DR	PRINTS; PR00404; MADSDOMAIN.			
DR	SMART; SM00432; MADS; 1.			
DR	PROSITE; PS00350; MADS_BOX_1; 1.			
DR	PROSITE; PS00650; MADS_BOX_2; 1.			
KW	DNA-binding; Nuclear protein; Transcription regulation.			
SO	SEQUENCE 248 AA; 28835 MW; 2470CDF92D708319 CMC64;			
Query Match 56.1%; Score 683; DB 10; Length 248;				
Best Local Similarity 70.3%; Pred. No. 2.2e-37;				
Matches 128; Conservative 32; Mismatches 22; Indels 0; Gaps 0;				
QY	1	MGRGVOLAKRIENKINROYTSKRKSGLLKKAHEISVLCDAEVALIVSSKCKLEFYSTD	60	
Db	1	MGRGVOLAKRIENKINROYTSKRKSGLLKKAHEISVLCDAEVALIVSSKCKLEFYSTD	60	
QY	61	SCMERITERYRYLYSDOLGVDSQSENNVLEHAKLKARVEYEKKRNPMFGDLSL	120	
Db	61	SCMDRIETERYRYSAEQLVSNFQSPANWLTLESLKARIELQRRNRHFMGDDLSM	120	
QY	121	SLKEIQLSLEHOLDAIKSIRSRKKNQAMFESISALQKDKALODHNNSLLKTIKEREKKTG	180	
Db	121	SLKEIQLSLEHOLDAIKSIRSRKKNQAMFESISALQKDKALODHNNSLLKTIKEREKKTG	180	
QY	181	QOEGQLVCCSNSSVLLPQ	199	
Db	181	QOEGQLVCCSNSSVLLPQ	199	

AC		09A813:	01-JUN-2001 (TREMBlrel. 17, Created)
DT		01-JUN-2001 (TREMBlrel. 17, Last sequence update)	
DT		01-MAR-2002 (TREMBlrel. 20, Last annotation update)	
DE	MADS-box transcription factor (MADS-box transcription factor MADS4).		
GN	PEAM4.		
OS	Pisum sativum (Garden pea).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots: Rosidae;		
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.		
OX	NCBITaxId=3868;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. VIKTORIA; TISSUE=FLORAL APICES;		
RA	Berbel A., Navarro C., Ferrandiz C., Canas L.A., Madueno F.,		
RT	Beltran J.P.;		
RT	"Analysis of PEAM4, the pea ApI functional homologue, supports a model		
RT	for ApI controlling both floral meristem identity and a function in		
RL	different plant species.";		
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. VIKTORIA;		
RX	MEDLINE=21159587; PubMed=11260500;		
RA	Berbel A., Navarro C., Ferrandiz C., Canas L.A., Madueno F.,		
RA	Beltran J.P.;		
RT	"PEAM4, the pea functional homologue to APETALA1 and SQUAMOSA, works		
RT	as an A-function gene.";		
RL	Plant J. 25:441-451(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Taylor S., Hofer J., Murfet I., Sollinger J., Singer S., Knox M.,		
RA	Ellis N.;		
RT	"Proliferating inflorescence meristem, a MADS-box gene that regulates		
RT	floral meristem identity in pea,"		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
CC	-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	-I- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.		
DR	EMBL: AJ279089: CAC37031.1; -		
DR	EMBL: AJ291298: CAC35027.1; -		
DR	EMBL: AF461740: AAL6379.1; -		
DR	HSSP: P11746: IMNM.		
DR	InterPro: IPR002487: TF_Kbox.		
DR	InterPro: IPR002100: TF_MADSbox.		
DR	pfam: PF01486: K-box_1		
DR	pfam: PF00319: SRP-TF; 1.		
DR	PRINTS: PR00404: MADSDOMAIN.		
DR	SMART: SM00432: MADS_1.		
DR	PROSITE: PS00350: MADS_BOX_1; 1.		
DR	PROSITE: PS00066: MADS_BOX_2; 1.		
KW	DNA-binding; Nuclear protein; Transcription regulation.		
QY	SEQUENCE 240 AA. 28184 MW. 653EAS8D05196216 CMC64:		
Query Match	55.8%; Score 680; DB 10; Length 240;		
Best Local Similarity	69.7%; Pred.No. 3.3e-37;		
Matches 129; Conservative 30; Mismatches 26; Indels 0; Gaps 0;			
QY	1 MGRGVQLKRIINRKINROYTFESKRSGLLKAHEISVLCDAEVALIVSSKKGLFEYSTD 60		
DB	1 MGRGVQLKRIINRKINROYTFESKRSGLLKAHEISVLCDAEVALIVSHKCKLFREYATD 60		
QY	61 SCMERLTLEKYDYELVSKDLVGADVDSQSENVWLHAHLKARVEVEKKRNRMGEDLSL 120		
DB	61 SCMEKILEYEYEAERVLAVANDESQGNWTETTRTLAKADLDLRNRHFMGDDLGTM 120		
QY	121 SLKELOSIEHQDLAAIKSIIRSRKNQAFESISALOKDKALODHNNSLLKTIKERKKTG 180		
DB	121 SLKELOSIEHQDLPAKLIRTRRNLWMVESTIEQKKKEVIGEQNNMLAKTKIKEREKTA 180		
QY	181 QOEQG 185		
DB	181 EQOVQ 185		

Search completed: January 27, 2003, 12:39:02  
Job time : 34 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 05:39:47 ; Search time 3036 Seconds  
(without alignments)  
10180.230 Million cell updates/sec

Title: US-09-981-087a-1

Perfect score: 1062

Sequence: 1 cccagagagacataagaag.....taatgattctcatgaata 1062

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: GenEmbl.\*  
2: gb\_da.\*  
3: gb\_htg.\*  
4: gb\_in.\*  
5: gb\_cm.\*  
6: gb\_ov.\*  
7: gb\_pat.\*  
8: gb\_ph.\*  
9: gb\_pl.\*  
10: gb\_pr.\*  
11: gb\_ro.\*  
12: gb\_sts.\*  
13: gb\_sy.\*  
14: gb\_un.\*  
15: gb\_vl.\*  
16: em\_da.\*  
17: em\_fun.\*  
18: em\_hum.\*  
19: em\_in.\*  
20: em\_mu.\*  
21: em\_om.\*  
22: em\_or.\*  
23: em\_ov.\*  
24: em\_pat.\*  
25: em\_ph.\*  
26: em\_pl.\*  
27: em\_ro.\*  
28: em\_sts.\*  
29: em\_un.\*  
30: em\_vl.\*  
31: em\_htg\_hum.\*  
32: em\_htg\_inv.\*  
33: em\_htg\_other.\*  
34: em\_htg\_mus.\*  
35: em\_htg\_pln.\*  
36: em\_htg\_rtd.\*  
37: em\_htg\_mam.\*  
38: em\_htg\_vrt.\*  
39: em\_sy.\*  
40: em\_htgo\_hum.\*  
41: em\_htgo\_mus.\*  
42: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1062	100.0	1062	6	ARI38344 Sequence
2	1062	100.0	1062	6	ARI50973 Sequence
3	1058	99.6	1058	8	ATU03473
4	1018	95.9	1042	8	AF386929 Arabidops
5	874	82.3	874	8	AY072463 Arabidops
6	710.8	66.9	946	8	SAU25695
7	345	32.5	61634	8	AB008269 Arabidops
8	339.8	32.0	966	8	BPAD55GN
9	322.4	30.4	1230	8	MDU78948
10	319.6	30.1	970	8	SLIM5
11	312.4	29.4	1085	8	AF305076
12	311.6	29.3	956	8	AF130118
13	311.2	29.3	1032	8	AF305696
14	311.2	29.3	1070	8	AF306349
15	310.2	29.2	1029	8	AF068725
16	309.8	29.2	1131	6	AB1451
17	309.8	29.2	1131	8	AF176782
18	309	29.1	1140	8	PSA279089
19	309	29.1	1207	8	AF461740
20	307.4	28.9	1062	8	STU23758
21	307.2	28.9	962	8	LETDR4
22	305.8	28.8	1068	8	STU23757
23	303.6	28.6	1023	8	SAAP1
24	303.2	28.5	998	8	BPAD54GN
25	302.6	28.5	1079	8	SCAF002666
26	301	28.3	794	6	AR042840
27	301	28.3	794	6	AR095091
28	301	28.3	794	6	AR111348
29	301	28.3	794	6	AR200415
30	301	28.3	1138	8	BOU67452
31	300.8	28.3	1143	8	AF009126
32	298.2	28.1	1050	8	AF109403
33	297.8	28.0	1051	8	BOBOAPIMR
34	296.8	27.9	1054	6	AR063254
35	296.8	27.9	1054	6	ATAP1
36	296.8	27.9	1057	6	AR095090
37	296.8	27.9	1057	6	AR200414
38	296.8	27.9	1165	8	AY087956
39	296.8	27.9	1215	6	AR042839
40	296.8	27.9	1215	6	AR111347
41	291.4	27.4	768	6	AR042841
42	291.4	27.4	768	6	AR095092
43	291.4	27.4	768	6	AR111349
44	291.4	27.4	768	6	AR200416
45	289.8	27.3	1142	8	BOU67451

#### ALIGNMENTS

RESULT 1  
LOCUS ARI38344  
DEFINITION Sequence 1 from patent US 6198024.  
ACCESSION ARI38344  
VERSION ARI38344.1 GI:14479853  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1062)  
AUTHORS Yanofsky,M.F. and Ferrandiz,C.  
TITLE Seed Plants characterized by delayed seed dispersal  
JOURNAL Patent: US 6198024-A 1 06-MAR-2001;  
FEATURES location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

source	1. .1062
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BASE COUNT	327 a	193 c	240 g	302 t
ORIGIN				

Query Match	100.0%;	Score 1062;	DB 6;	Length 1062;
Best Local Similarity	100.0%;	Pred. No. 1.1e-228;		
Matches 1062; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	CCACAGAGACATAGAAAGAAAGAGAGAGACATCTTTGGTCATTTCCAGGGTTGCG	60
Db	1	CCACAGAGACATAGAAAGAAAGAGAGAGAGACTCTTTGGTCATTTCCAGGGTTGCG	60
QY	61	TTTCTCTCTTGTCTTGTAGATTTTGAAGAGAGACATATGGGAAGAGGTAGCGTTCA	120
Db	61	TTTCTCTCTTGTCTTGTAGATTTTGAAGAGAGACATATGGGAAGAGGTAGCGTTCA	120
QY	121	GCTGAAGAGATAGAAACAAGATCAATAGCCAGTTACTTTCTCMAAGAGAGCTGCG	180
Db	121	GCTGAAGAGATAGAAACAAGATCAATAGCCAGTTACTTTCTCMAAGAGAGCTGCG	180
QY	181	TTTGGTCAAGAAAGCTATGAGATCTCGTCTCGGCAATGCTAGAGTTGCTCTCATCGT	240
Db	181	TTTGGTCAAGAAAGCTATGAGATCTCGTCTCGGCAATGCTAGAGTTGCTCTCATCGT	240
QY	241	CTTCTCTTCCAAAGGCCAAACCTCTTCGAATTTTCCAGCCAGCTCTTGACATGAGAGATAC	300
Db	241	CTTCTCTTCCAAAGGCCAAACCTCTTCGAATTTTCCAGCCAGCTCTTGACATGAGAGATAC	300
QY	301	TGAACGCTATGATGGCTATTTATATTCAGACAAACACTTGTGGCCGAGACGTTTACA	360
Db	301	TGAACGCTATGATGGCTATTTATATTCAGACAAACACTTGTGGCCGAGACGTTTACA	360
QY	361	AAGTGAATAATTTGGGTTCTAGAAACATGCTCAAGCCAGAGAGTTGAGACTTTGAGAA	420
Db	361	AAGTGAATAATTTGGGTTCTAGAAACATGCTCAAGCCAGAGAGTTGAGACTTTGAGAA	420
QY	421	GAACAAAGAAATTTTATGGGGGAAAGATCTTGATTCGTTGAGCTTGAAGAGACTCCAAG	480
Db	421	GAACAAAGAAATTTTATGGGGGAAAGATCTTGATTCGTTGAGCTTGAAGAGACTCCAAG	480
QY	481	CTTGGAGATACGCTCGATGACGCTATCCAAAGCATTAAGTTCAGAGAAAGAACCAAGCTAT	540
Db	481	CTTGGAGATACGCTCGGATGACGCTATCCAAAGCATTAAGTTCAGAGAAAGAACCAAGCTAT	540
QY	541	GTTCGAATCCATATCTCGGCTCCACAGAAAGATTAAGCCCTTGCAGATCCACAATATTC	600
Db	541	GTTCGAATCCATATCTCGGCTCCACAGAAAGATTAAGCCCTTGCAGATCCACAATATTC	600
QY	601	GCTTCTCAAAAAGATTTAAGAGAGAGGAGAGAAAAAGGGTCCAGCAAGAGACATTAAGT	660
Db	601	GCTTCTCAAAAAGATTTAAGAGAGAGGAGAGAAAAAGGGTCCAGCAAGAGACATTAAGT	660
QY	661	CCATAGCCCAACCTCTTCTAGTTCTTCCGCCATATCTGCGCTAACCTCTCCAAAGA	720
Db	661	CCATAGCCCAACCTCTTCTAGTTCTTCCGCCATATCTGCGCTAACCTCTCCAAAGA	720
QY	721	TGGCTTTGTGAGAGAGATTTGGGGAGAGAACGGTGGTGCATCGCTGTGACGGAGAACAA	780
Db	721	TGGCTTTGTGAGAGAGATTTGGGGAGAGAACGGTGGTGGTGCATCGCTGTGACGGAGAACAA	780
QY	781	CTCTCTGCTTCGCGCTTGAGATGTTACGTCCTACCATTCAGAACGAGTAGAAGTAATCTCAC	840
Db	781	CTCTCTGCTTCGCGCTTGAGATGTTACGTCCTACCATTCAGAACGAGTAGAAGTAATCTCAC	840
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AR150973

LOCUS	ARI50973	1062 bp
DEFINITION	Sequence 1 from patent US 6229068.	
ACCESSION	ARI50973	
VERSION	ARI50973.1	GI:15115564

SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.

REFERENCE  
1 (bases 1 to 1062)  
AUTHORS  
Yanofsky, M.F., Martienssen, R., Ferrandiz, C. and Gu, Q.  
METHOD  
Method of increasing fruit size

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ORIGIN				

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			Gaps	0

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Dp	61	TTTCTCTCTTGGTCTTGAAGATTTTGAAGAGAGAGATTTGGAGAGGTAGGGTTCA	120
QY	121	GCTGAGAGGATAGAGAACAAAGATCAATAGGCAAGTTACTTTCTCAAGAGAAAGCTGCG	180
Dp	121	GCTGAGAGGATAGAGAACAAAGATCAATAGGCAAGTTACTTTCTCAAGAGAAAGCTGCG	180
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Dp	181	TTTGGTCAAGAAAGCTCATGAGATCTCTGTTCTGGGATCTGAGGTTCTCTCATCGT	240
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Dp	241	CTTCTCTTCCAAAGGCAAACTCTTCGAATATTCACCGACCTCTTGCATGAGAGGATACT	300
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Dp	301	TGAAGCGTAGATGCGTATTTTATATTCAGACAAACACTTGTGGCCGACGCTTTTACA	360
QY	361	AAGTGAATTTGGGTTCTAGAACATGCTAAAGCTCAAGGCAAGGTTGAGTACTTAGAA	420
Dp	361	AAGTGAATTTGGGTTCTAGAACATGCTAAAGCTCAAGGCAAGGTTGAGTACTTAGAA	420
QY	421	GAAACAAAAGGAATTTTATGGGGGAAGTCTTGATTCGTTAGCGTTGAAGAGCTCCAAAG	480
Dp	421	GAAACAAAAGGAATTTTATGGGGGAAGATCTTGATTCGTTAGCGTTGAAGAGCTCCAAAG	480
QY	481	CTTGGAGCATCAGCTCGATGCACTAATCAAGAGCATTTAGSTCAAGAAAGACCAAGCTAT	540
Dp	481	CTTGGAGCATCAGCTCGATGCACTAATCAAGAGCATTTAGSTCAAGAAAGACCAAGCTAT	540
QY	541	GTTGGAATCCATATCTCGGCTCCGAGAAAGAGATAAAGCCTTCAGATCACAAACAATC	600
Dp	541	GTTGGAATCCATATCTCGGCTCCGAGAAAGAGATAAAGCCTTCAGATCACAAACAATC	600



Qy 601 GCTTCTCAAAAAGATTAAAGAGAGGAGAGAAAAGGGCTGACGACAGAAGCAATTAGT 660  
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Db 1021 AGAACAAAGATTCTATCTTGTGTAATGATTTCTCTATGAAATA 1062

RESULT 3  
AFU3473

LOCUS 1058 bp mRNA linear PLN 17-APR-1996  
DEFINITION Arabidopsis thaliana agamous-like 8 (AGL8) mRNA, complete cds.  
ACCESSION U33473  
VERSION U33473.1 GI:1004364  
KEYWORDS

## SOURCE

Arabidopsis thaliana.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

## REFERENCE

1 (bases 1 to 1058)  
Mandel, M.A. and Yanofsky, M.F.  
The Arabidopsis AGL8 MADS box gene is expressed in inflorescence  
meristems and is negatively regulated by APETALA1

## AUTHORS

Mandel, M.A. and Yanofsky, M.F.

## JOURNAL

Plant Cell 7 (11), 1763-1771 (1995)

## MEDLINE

96093419

## PUBMED

8535133

## REFERENCE

2 (bases 1 to 1058)  
Mandel, M.A. and Yanofsky, M.F.  
Direct Submission  
Submitted (09-AUG-1995) M. Alejandra Mandel, Biology, University of  
California at San Diego, La Jolla, CA 92093-0116, USA

## FEATURES

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CDS

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ORIGIN

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Db	1021	AGACAAGATTCATATCTTGGTAAATGATTTCTCAGCA	1058
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LOCUS	AF386929	Arabidopsis thaliana floral homeotic protein AGL8 (MSL3.3)	mrna, linear
DEFINITION		complete cds.	
ACCESSION	AF386929.1	GI:14423383	
VERSION		FL1_CDNA.	
KEYWORDS		Arabidopsis thaliana.	
SOURCE		Arabidopsis thaliana	
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
REFERENCE		1 (bases 1 to 1042)	
AUTHORS		Lam,B., Southwick,A., Karlin-Neumann,G., Nguyen,M., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamlya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.	
TITLE		Direct Submission	
JOURNAL		Submitted (30-MAY-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA	
COMMENT		e-mail for correspondence: arab@sequence.stanford.edu	
		RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamlya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.	
		The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Lam,B., Karlin-Neumann,G., Nguyen,M., Southwick,A., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.	
		Lam,B., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.	
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RESULT 5  
LOCUS AY072463  
DEFINITION Arabidopsis thaliana floral homeotic protein AGU8 (MSL3.3) mRNA,  
complete cds.  
ACCESSION AY072463  
VERSION AY072463.1 GI:18377423  
KEYWORDS FLI, CDNA.  
SOURCE Arabidopsis thaliana.  
ORGANISM Arabidopsis thaliana.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 874)

REFERENCE  
AUTHORS Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M.,  
Palm, C. J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H.,  
Cheuk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, A.,  
Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P. K.,  
Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K.,  
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R. W.  
Direct Submission  
Submitted (02-JAN-2002) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA  
e-mail for correspondence: arab@sequence.stanford.edu

COMMENT  
Riken Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,  
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y. and Shinozaki, K.

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RESULT 6  
LOCUS SAU25695  
DEFINITION Synapsis alba transcription factor SAMADS B mRNA, complete cds.  
ACCESSION U25695  
VERSION U25695.1 GI:1049023  
KEYWORDS  
SOURCE Synapsis alba.  
ORGANISM Synapsis alba



http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).  
Genes encoding tRNAs are predicted by tRNAscan-SE  
(Sean Eddy, Washington University School of Medicine, St. Louis,  
http://genome.wustl.edu/eddy/tRNAscan-SE/).  
This sequence may not be the entire insert of this clone. It may be  
shorter because we remove overlaps between neighboring submissions.  
The 5' clone is MAF1 and the 3' clone is MAF19.

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Query Match      32.5%: Score 345: DB 8: Length 61634:
Best Local Similarity 100.0%: Pred. NO. 1.6e-67:
Matches 345: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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RESULT 8				
BPMAD55GN				
LOCUS	BPMAD55GN	966 bp	mRNA	linear
DEFINITION	B.pendula mRNA for MAD5 box protein, MAD55.			
ACCESSION	X99655			
VERSION	X99655.1	GI:1483231		
KEYWORDS	MAD5 box protein; MAD55 gene.			
SOURCE	European white birch.			
ORGANISM	Betula pendula			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
TITLE	Rosidae; eurosids I; Fagales; Betulaceae; Betula.			
	1 (bases 1 to 966)			
	Eio,A., Lemmetyinen,J., Turunen,M.L., Tikka,L. and Sopanen,T.			
	Three MAD5 box genes homologous to <i>SQUAMOSA</i> and <i>APETALA1</i> have			
	different expression patterns in silver birch ( <i>Betula pendula</i>			
	Roth.)			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 966)			
AUTHORS	Eio,A.			
TITLE	Direct Submission			
JOURNAL	Submitted (30-JUL-1996) A. Eio, University Of Joensuu, Department			
	Of Biology, P.O. Box 111, 80101 Joensuu, FINLAND			
FEATURES	Location/Qualifiers			
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Db	122	AGGCAGGTCACCTTTCACAGAGAGCGGTACAGGTTGCTGGAAGAAAGCCCATGAGATCTCT	181
QY	209	GTTCTCTGGGATGCTGAGGTTGCTCTCATCGTCTCTCTCTCCAAAGGCAAACTCTTCGAA	268
Db	182	GTGCTTTGTATGATGAGGAGGCTTGATGTCTCTCCACCAAGGAAAGCTCTTTGAG	241
QY	269	TATTCACCGCAGCTCTGCATGGAGAGGATACTTGAACGCTATGATCGCTATTTATATTC	328
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QY	329	GACAAACAACTTTGTTGGCCGAGAACGCTTTCACAAAGTGAATAATTTGGGTTCTAGAACATGCT	388
Db	302	GACAGGAGATCTTCTTCAATATCTTGAAACAAATGGAAAGCTGACCTCTGGAAACATGCA	361
QY	389	AAGCTCAAGGCAAGAGATTGAGTACTTGATGAGAAGAACAAAGAGATTTATGGGGAGAAAT	448
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QY	449	CTTGATTCGTGAGCTTGGAAGAGCTCCAAAGCTTTGGAGCATCAGCTCGATATGCACTATTC	508
Db	422	CTGATTCCTCTTGAGTCTTAAAGAGCTTCAAATAATTTGGAGCAACGCTTGATTCGCTTCC	481
QY	509	AAGAGCATTAATGCAAGAAAGAACCAACGCTATTTGTCGATTCATATGCTGGCTCCAGAG	568
Db	482	AAACACATCNGGTCAAGAGAGAACCAACTTATGTACGATTCGATTTAGAGCTTCCAGACA	541
QY	569	AAGGATTAAGCCTTGCAGAGATCACAACAATTCGCTCTCCAAAAGGATTAAAGAGAGGAG	628
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QY	629	AAGAAACGGGTCAGCAAG 647	
Db	602	AAGGAATTAGCCCAACAG 620	
RESULT 9			
LOCUS	MDU78948		
DEFINITION	MDU78948	1230 bp	mrna
ACCESSION	U78948		linear
VERSION	U78948.1		PLN 26-AUG-1999
KEYWORDS			
SOURCE	Malus x domestica.		
ORGANISM	Malus x domestica		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		





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Db	262	ACTGCACCGATTC	CGATTCTCATCTTACTG	AGCTTTGGAGAC	TGCTTAAGCGCT	321
OY	401	ACAGTTGAGCTACT	TGAGAGAAACAAAGGATTTATGGG	GAACATGTCATTGCT	GTG	460
OY	322	ACACTTGAATTT	CACAGAGATCTATAGC	ATTATATGGGGAAGATCTA	GTACTTACCTTG	381
Db	461	ACCTTGAAGAGCT	CCAAAGCTTTGGAGCATGAC	TGACATGACATTAAG	CACTTAGG	520
Db	382	ACTTTGAAGAGCT	CTCAGAAATTTGCAACATCA	ACTGACATGCTTTAA	CACATCCGA	441
OY	521	TCAAGAAAGACCA	AGCTATGTTGCAATCATAT	TGCGCTCCAGAGAAG	ATTAAGCC	580
Db	442	TCCAGAAAGAAC	CCAGCTCATGTACGAATTA	ATTAATTCAGACGCT	TCAGAAAGACA	501
OY	581	TTGCAAGATCA	CAACAATTCGCTTCCAAAAGATTA	AGSAGAGAGAAACGG	CT	640
Db	502	TTGCGAGACAT	TAACATACCTATCAAGAAAGGTGA	AGAGAGAGAGAAAG	GAAGAA	561
OY	641	CAGCAAGAAG	650			
Db	562	AAGGAAAGG	571			
RESULT	11					
LOCUS	AF305076	1085 bp	mRNA	linear	PLN 23-OCT-2000	
DEFINITION	Eucalyptus globulus MADS-box protein EAP1 mRNA, complete cds.					
ACCESSION	AF305076					
VERSION	AF305076.1	GI:10946428				
KEYWORDS						
SOURCE						
ORGANISM	Eucalyptus globulus.					
	Eucalyptus globulus					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Myrtales; Myrtaceae; Eucalyptus.					
REFERENCE	1 (bases 1 to 1085)					
AUTHORS	Kyozuka,J., Harcourt,R., Peacock,W.J. and Dennis,E.S.					
TITLE	Eucalyptus has functional equivalents of the Arabidopsis AP1 gene					
JOURNAL	Plant Mol. Biol. 35 (5), 573-584 (1997)					
MEDLINE	98009992					
PubMed	9349279					
REFERENCE	2 (bases 1 to 1085)					
AUTHORS	Kyozuka,J., Harcourt,R., Peacock,W.J. and Dennis,E.S.					
TITLE	Direct Submission					
JOURNAL	Submitted (12-SEP-2000) Plant Industry, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia					
FEATURES	Location/Qualifiers					
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Best Local Similarity	70.8%;	Pred. No. 5e-60;				
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Dd	68	TTTGGCGGTGCTTGTTGGTTGGTAATTGGAGCGAGATGGGAGGGAGGCCTCCAG	127
Oy	122	CTGAAGAGGATAGAAACAAGATCAATPAGCAAGTTACTTCTCAGAAGAGGCTGGT	181
Dd	128	CTGAAGAGGATAGAAACAAGATCAACCGCAAAATCACCTTCCTCCAGAGAGGCGGGT	187
Oy	182	TTCGTCAGAAGAGCTCATGAGATCTCTGTTCTCTCGATGCTGAGGTTGCTCTATCTC	241
Dd	188	CTGCTCAAGAAGGCCACGAGATCTCCGTCCTCGTCGAGCGCCGAGGTCGCCCTATCTC	247
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Dd	248	TTTCTCCGCCAAGGGCAAGCTCTTCAGATCTCCACCAGATTTCTCTCATGAGAGATTTCTC	307
Oy	302	GAAAGCATGATGCGCTATTATTAATTCAGAACAAACAATTGTTGGCCGAGACGTTTCA	361
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Dd	368	ATTGGTAGCTGGACCTTTGGAGCTGCTTAAGCTCAAGGCGCAACTGTGAAGTTTACAC	427
Oy	422	AACAAAGAAATTTTTTTGGGGGAAAGATCTTGAATGCTTGAGCTTGAAGAGCTCCAA	481
Dd	428	AATATATGAGCATTTCCATGGAGAAAGATCTTGATTTCTTTGAGTCTCAAGAGCTCC	487
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Dd	488	TTGAGCAGCAACATCGAGATCTGCTTTAAACATATAGATGAGAAAGATCAGCTCAG	547
Oy	542	TTGCAATCCATATCTCGCTCCAGAAAGATTAAGCTTGCAGAAATCCAAACATTTG	601
Dd	548	CATCAATCAATCTCAGCTCTCGAGAAAAAGGATGAGGATTTGCAGGAGCAAAATTA	607
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Dd	608	CTTCAAAAGAAATTAAGGAGAGGAGAGGCGCATAGCACAGCAAG	653
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RESULT_12			
AF130118			
LOCUS	AF130118	956 bp	mRNA linear PLN 21-JUN-2001
DEFINITION	CapSicum annuum MADS box protein (MAD5) mRNA, complete cds.		
ACCESSION	AF130118		
VERSION	AF130118.2	GI:14518446	
KEYWORDS	.		
SOURCE	CapSicum annuum.		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatidae; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.		
REFERENCE	1 (bases 1 to 956)		
AUTHORS	Sung,S.-K., Moon,Y.-H., Chung,J.-E., Lee,S.-Y., Park,H.G. and An,G.		
JOURNAL	Characterization of MADS box genes from hot pepper		
MEDLINE	Mol. Cells 11 (3), 352-359 (2001)		
PUBMED	21351847		
REFERENCE	2 (bases 1 to 956)		
AUTHORS	Jung,J.-Y., Moon,Y.-H., Chung,J.-E., Sung,S.-K. and An,G.		
JOURNAL	Direct Submission		
TITLE	Submitted (20-FEB-1999) Department of Life Science, POSTECH, San		
REFERENCE	31, Hyoja-dong, Nam-gu, Pohang 790-784, Republic of Korea		
AUTHORS	(bases 1 to 956)		
JOURNAL	Jung,J.-Y., Moon,Y.-H., Chung,J.-E., Sung,S.-K. and An,G.		
TITLE	Direct Submission		
REMARK	Submitted (21-JUN-2001) Department of Life Science, POSTECH, San		
COMMENT	31, Hyoja-dong, Nam-gu, Pohang 790-784, Republic of Korea		
FEATURES	Sequence update by submitter		
SOURCE	On Jun 21, 2001 this sequence version replaced gi:6651034.		
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Db 722 CACAGCAA 729

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RESULT 14

AF306349 1070 bp mRNA linear PLN 08-NOV-2000

LOCUS Eucalyptus globulus MADS box protein AP2L mRNA, complete cds.

DEFINITION AF306349

AF306349 AF306349.1 GI:11120556

VERSION

KEYWORDS

SOURCE Eucalyptus globulus.

ORGANISM Eucalyptus globulus.

REFERENCE 1 (bases 1 to 1070)

AUTHORS Kyozuka, J., Harcourt, R., Peacock, W.J. and Dennis, E.S.

TITLE Eucalyptus has functional equivalents of the Arabidopsis AP1 gene

JOURNAL Plant Mol. Biol. 35 (5), 573-584 (1997)

MEDLINE 98009992

PUBMED 9349279

REFERENCE 2 (bases 1 to 1070)

AUTHORS Kyozuka, J., Harcourt, R., Peacock, W.J. and Dennis, E.S.

TITLE Direct Submission

JOURNAL Submitted (15-SEP-2000) Plant Industry, CSIRO, GPO Box 1600, Canberra, ACT 2601, Australia

FEATURES

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BASE COUNT 309 a 240 c 269 g 252 t

ORIGIN

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Best Local Similarity 73.0%; Pred. No. 9.4e-60;

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Db 182 AAATGGGGAGGGGAGGGGAGGCTGAAGAGATAGAGAACAATGATAGGCAAGTTA 241

QY 159 GTTCTCAAGAGAGAGGTCGTGCTCAAGAGAGATGATGATGATGCTGCTGCGG 218

Db 242 CGTTTCGAAGGGAGATGCGGGCTGCTGAAGAGGCCACGAGATCGCTCTGCG 301

QY 219 ATGCTAGAGTTGCTCTCATGCTCTCTCTTCCAAAGGCAAACTCTGCAATATTCACAGC 278

Db 302 ACGCGAGCTGCGCCCTCATGCTCTCTCCACCAAGGCAAGCTCTCGATGCGCCAGC 361

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Db 362 ACTGTTCATGAGAGAGATCTCGAGCGCTTATGAGATATTCATATGCAAGAGACAG 421

QY 339 TTGTTGGCCGAGAGCTTTCACAAAGTGAATGGAATTTGGTCTAGAACATGCTCAAG 398

Db 422 TTCTTCACAAACATGCCCAACCAATGGAGACTGGACTTGGAACTGCAAACTCAAG 481

QY 399 CAAGATGAGTACTTGAAGAGAAACAAGAAATTTATGGGGGAAGATCTTGATTCGT 458

Db 482 CCAGAGTGAAGATCTTGCAAGAAATCAAAAGATCTGATGGAGAGAAGAACTGATTCG 541

QY 459 TGAGCTTAAGAGAGCTCCAAAGCTTGAGACATCAGCTCATGACGATCAAGAGCATT 518

Db 542 TAAGCCTCAAGAGCTTCGAATTTGGAGCATCAGCTGACATCGCTCTTAAGAACATTTC 601

QY 519 GGTCAAGAAAGAACCAAGCAAGTATGTTGCAATCCATATCTCGCGTCCGAGAAAGATTAAG 578

Db 602 GGTCTGAAAGATTCATCACTCATGTGATTCATCTCTAGACTTCAGAGAAAGATTAAG 661

QY 579 CCTTGCAGATCAACAATTCGCTTCTCAAAAAGATTAGAGAGAGGAGAAAGAACGG 638

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QY 639 GTCAAGCA 646

Db 722 CACAGCAA 729

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RESULT 15

AF068725 1029 bp mRNA linear PLN 16-JUN-1999

LOCUS Nicotiana sylvestris MADS-box protein MADS1 (NSMADS1) mRNA, complete cds.

DEFINITION AF068725

AF068725 AF068725.1 GI:5070141

ACCESSION

KEYWORDS

SOURCE Nicotiana sylvestris.

ORGANISM Nicotiana sylvestris.

REFERENCE 1 (bases 1 to 1029)

AUTHORS Jiang, S. and An, G.

TITLE NSMADS1, a member of the MADS gene family from Nicotiana sylvestris

JOURNAL J. Plant Biol. 42 (1), 85-87 (1999)

REFERENCE 2 (bases 1 to 1029)

AUTHORS Jiang, S. and An, G.

TITLE Direct Submission

JOURNAL Submitted (28-MAY-1998) Department of Life Science, Pohang University of Science and Technology, San 31 Hyojadong, Pohang, Kyungbuk 790 - 784, Korea

FEATURES

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polyA\_site 1020

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BASE COUNT 340 a 189 c 216 g 284 t

ORIGIN

Query Match 29.2%; Score 310.2; DB 8; Length 1029;

Best Local Similarity 69.2%; Pred. No. 1.6e-59;

Matches 423; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

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Db 14 ATCACTGATCTTGTGACAGCTTATGATCTCTCTCTCTCTGCTGAATAATTAATTT 73



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PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
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Matches 1057; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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Qy	852	TATATGATATATATTAATGTTTAAATTTTTCATACATTCAGATTTTGGTACTT	911
Db	241	TATATGATATATATTAATGTTTAAATTTTTCATACATTCAGATTTTGGTACTT	300
Qy	912	ATACATATTAATTAATACGATATGTTTACCTAGCTATCATATTAATGATGTAACCTC	971
Db	301	ATACATATTAATTAATACGATATGTTTACCTAGCTATCATATTAATGATGTAACCTC	360
Qy	972	GTTTGTGAGACGTATGATACGTATACGTATCATATTAATGATGTAACCAAGAT	1031
Db	361	GTTTGTGAGACGTATGATACGTATACGTATCATATTAATGATGTAACCAAGAT	420
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ID	AAT34430 standard; cDNA; 1032 BP.		
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AC	01-OCT-1996 (first entry)		
DT	Eucalyptus, SOE2S cDNA.		
DE	Eucalyptus; reproductive gene; SOE2S; Arabidopsis; agamous gene;		
KM	Antirrhinum; plena gene; sterility; fertility; forest tree;		
KM	transgenic plant; flower development; antisense; ribozyme; ss.		
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FT	Location/Qualifiers		
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PI	Peacock WJ, Southerton S;		
PI	WPI; 1996-278411/29.		
XX	P-PSDB; AAR9635.		
DR	Eucalyptus reproductive genes - useful for prodn. of sterile		
PT	Eucalyptus trees useful for establishing wood lot plantations or in		
PT	re-forestation projects		
PS	Claim 8; Page 34-35; 60pp; English.		
CC	cDNA clones SOE1 (AAT34429), SOE2S (AAT34430) and SOE2L (AAT34431) were		
CC	identified by homology to the MADS box of the Arabidopsis apetala		
CC	1 (AP1) and Antirrhinum squamosa (SQUA) flower development genes.		
CC	They were obtd. by PCR amplification of E. globulus DNA using		
CC	primers based on the MADS box of the Arabidopsis and Antirrhinum		
CC	genes, followed by screening of a E. globulus young flower bud		
CC	library. The SOE2S cDNA codes for protein SOE2-S (AAR9635).		

CC Antisense or ribozyme constructs of SQE, or of FLE2 and SQE genes  
CC (see also ANT34446, ANT34428 and ANT34432), may be used to produce  
CC sterile transgenic *Eucalyptus* trees by minimising inflorescence.  
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SQ Sequence 1032 BP; 299 A; 231 C; 263 G; 239 T; 0 other;

Query Match	29.6%	Score 314.4	DB 17	Length 1032
Best Local Similarity	73.4%	Pred. No. 1.1e-70		
Matches 402; Conservative	0	Mismatches 146	Indels 0	Gaps 0

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	Db	422	TTCACACAAACCAATGCGGAAACCAATGCGAATCGACTTTGGAAACATGCAAAACCTCAAG	481
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	Db	482	CCAGGATGGGAGATTCTCCAGAAAAATCCAAAAGATCTGATGGGGAAGAACTCGATTCTC	541
	OY	459	TGACCTTGAAGGAGCTCCAAAAGCTTTGGAGCATAGCTCGATGCGCATCAAGAGCATTA	518
	Db	542	TAACTCTCCTCAAGAGCTTCAGAAATTTGGAGATCAGCTTGACACTGCTCTTAGAACATTC	601
	OY	519	GGTCAAGAAAGAACCAAGCTATGTTCCAAATCCATATCTGCGCTCCAGAAAGAGATPAAG	578
	Db	602	GGTCTAGAAAGATTCAACCTCATGTGTGTAATCCATCTCTGAACTTCAGAGAAAGATPAAG	661
	OY	579	CTTTGCAAGATCACACAAATTCGCTTCTCAAAAAGATTAAAGAGAGGAGAGACAAACGG	638
	Db	662	CGCTGCAAGAACCAAAACACATGCTGTGCAAAAGAAAGTGAAGAGAGAGAGAGCACTGG	721
	OY	639	GTCAGCAA	646
	Db	722	CACAGCAA	729
RESULT				
		6		
	AAT34429			
ID	AAT34429	standard;	cdNA; 1084 BP.	
XX	AAT34429:			
DT	01-OCT-1996	(first entry)		
DE	Eucalyptus SOE1 cdNA.			
KW	Eucalyptus; reproductive gene; SOE1; Arabidopsis; agomous gene;			
KM	Antirrhinum; plena gene; sterility; fertility; forest tree;			
XX	transgenic plant; flower development; antisense; ribozyme; ss.			
OS	Eucalyptus globulus.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	107..841		
FT		/+tag= a		
XX		/product= SOE-1		
	AU9539013-A			

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XX 30-MAY-1996.
PD 22-NOV-1995; 95AU-0039013.
XX 22-NOV-1994; 94AU-0009589.
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PI Dennis ES, Harcourt RL, Kyozeuka J, Llewellyn D;
PI Peacock WJ, Southern S.
XX MPI: 1996-278411/29.
XX P-PSDB: AAR99634.
XX Eucalyptus reproductive genes - useful for prodn. of sterile
XX Eucalyptus trees useful for establishing wood lot plantations or in
XX re-forestation projects
XX Claim 8; Page 31-32; 60pp; English.
XX cDNA clones SOE1 (AAT34429), SOE2S (AAT34430) and SOE2L (AAT34431) were
XX identified by homology to the MADS box of the Arabidopsis apetala
XX 1 (AP1) and Antirrhinum squamosa (SQUA) flower development genes.
XX They were obtd. by PCR amplification of E. globulus DNA using
XX primers based on the MADS box of the Arabidopsis and Antirrhinum
XX genes, followed by screening of a E. globulus young flower bud
XX library. The SOE1 gene contains a MADS box with 95% homology
XX to AP1 and 91% homology to SQUA. Its predicted amino acid
XX sequence is given in AAR99634. Antisense or ribozyme constructs of
XX SOE or of FLE2 and SOE genes (see also AAT34426, AAT34428 and
XX AAT34432), may be used to produce sterile transgenic Eucalyptus trees by
XX minimizing inflorescence.
SQ Sequence 1084 BP; 297 A; 258 C; 251 G; 278 T; 0 other;

Query Match 29.4%; Score 312.4; DB 17; Length 1084;
Best Local Similarity 70.8%; Pred. No. 3.8e-70;
Matches 415; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

OY 62 TTCTCTCTCTGTTCTTGAAGATTTTGAAGAGAGAGATATMGGAAGAGGTAGGCTCAG 121
DB 68 TTTTGGCGTGTGTGTTGGTGTGTGTAATTGGACCGAGATGGGAGGGAGGCTCAG 127
OY 122 CTGAAGAGATAGAGAACAAGATCAATVAGCAAGTACTTCTCAAGAGAGAGTCTGT 181
DB 128 CTGAAGAGATAGAGAACAAGATCAACCAAGTCACTTCTCAAGAGAGAGGCGGT 187
OY 182 TTGCTCAAGAGAGTATGATCTCTGTCTCGCATGCTGAGTGTCTCTCATGCTC 241
DB 188 CTGCTCAAGAGAGCCACGAGATCTCGTCTCGCAGCCCGAGGTCGCTCATGCTC 247
OY 242 TTCTCTTCAAGAGCAACTCTTCAAGATATTTCCACGACTCTTGCATGAGAGATCTT 301
DB 248 TTCTCGCCCAAGGCAAGCTCTTCAAGTACTTCCACGACTTCTGATGAGAGATCTC 307
OY 302 GAAAGCTATGATGCTATTATATATTCAGACAAACAATTGTGGCCGACGTTTCAACA 361
DB 308 GAAAGCTATGAAAGATCACTATATGCGGAGCACCACCAAGTCTTGAAGCGAGAGATCG 367
OY 362 AGTGAATAATGGGTCTTAGAAGATGCTAAGCTAAGGCAAGAGTGTGAGTCTGAGA 421
DB 368 ATTGGTAGCTGACTTTGGAGCATGCTAAGCTCAAGCCGAGCTTGAAGTTTACACAGA 427
OY 422 AACAAAGCAATTTATGAGGGAAGATCTGATTCGTGAGTGAAGAGGCTCCAAAGC 481
DB 428 AATTATAGCATTTTATGAGGCAAGATCTTGAATCTTGTGCTCAAGGACCTCCAAAT 487
OY 482 TTGAGCATCAAGCTGAGTATCAAGAGATTAAGTCAAGAGAGAGCAAGTATG 541
DB 488 TTGAGCAGCAACTGAGTCTGCTTAAACACATAGATCGAAGAAAGATTCAGCTATG 547
OY 542 TTGGAATCATATCTGCGCTCCAGAAAGAGATTAAGCTTGAAGATCAACAATTCG 601
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DB 548 CATGAATCAATCTCAGTATTCAGAAAAAGCATGGCATTCGAGGCAAAATTAACCTG 607
OY 602 CTTTCCAAAAAGATTAAAGAGAGAGAGAGAGAAAAAGGGTACAGAG 647
DB 608 CTTTCAAAAGAAATTAAGAGAGAGAGAGAGGCGCTAGCACAGCAG 653

RESULT 7
AAC55901
ID AAC55901 standard; DNA: 1223 BP.
XX AAC55901;
XX 25-JAN-2001 (first entry)
XX Eucalyptus grandis transcription factor DNA sequence #32.
XX DE
XX XX
XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
XX KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
XX KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox;
XX KW homeodomain zipper; LIM domain; AP2; ERBS; zinc finger domain;
XX KW type 2 Cys2His2; CCAAT box element; MYB; ss.
XX Eucalyptus grandis.
XX OS
XX WO200053724-A2.
XX PN
XX 14-SEP-2000.
XX PD
XX 09-MAR-2000; 2000WO-0506112.
XX PF
XX 11-MAR-1999; 99US-0266513.
XX PR 18-AUG-1999; 99US-0149485.
XX XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX PI Wood M, McGrath A, Shenk MA, Glenn M;
XX DR WPL; 2000-579369/54.
XX XX
XX New isolated polynucleotide encoding a plant transcription factor for
XX PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
XX PT having modified gene expression or modified activity of a polypeptide
XX PT -
XX XX
XX Claim 1; Pages 51-52; 747pp; English.
XX PS
XX The present invention relates to novel plant transcription factors from
XX CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
XX CC sequence for one such transcription factor. The transcription factor may
XX CC be used to produce a plant having modified gene expression such as a
XX CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
XX CC mahogany species or to modify the activity of a polypeptide in a plant.
XX CC The transcription factors of the present invention are members from the
XX CC following families of regulatory proteins: bZIP, bZIP family of G-box
XX CC binding factors, basic helix-loop-helix zipper,
XX CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
XX CC and ERBS, zinc finger domains of type 2 Cys2His2, CCAAT box elements
XX CC and MYB.
XX XX
SQ Sequence 1223 BP; 334 A; 292 C; 283 G; 314 T; 0 other;

Query Match 29.4%; Score 312; DB 21; Length 1223;
Best Local Similarity 71.4%; Pred. No. 5e-70;
Matches 411; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

OY 72 TGTCTTGAATTTTGAAGAGAGAGATATGGAAGAGTGGGTTCAGTGAAGAGA 131
DB 170 TGTGTTGGGTGTTGTAATTTGAGCAGAGATGGGAGGAGACTGCAGCTGAAGAGA 229
OY 132 TAGAGAACAAAGATCAATAGGCAAGTACTTCTCAAGAGAGAGTCTGTTGCTCAAGA 191
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||||| 230 TAGAACAAGATCAACCGCAAGTCACTCTCCAAAGAGAGGGGGTGTCTCAGA 289  
 OY 192 AAGCTCATGAGATCTCTGTCTCTCGATGAGTGTCTCTCATCTCTCTTCTCA 251  
 Db 290 AGGCCACAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 349  
 OY 252 AAGCAAACTCTTCGAATATTCACCGACTCTTGATGAGAGAGTACTTGAACGCTATG 311  
 Db 350 AGGGCAAGCTCTTCGAGTACTCTACCGATTCCTGCATGAGAAATTTCTCGAACGCTATG 409  
 OY 312 ATCGCTATTTATATTCAGACAACAACACTGTGTGGCCGAGCGCTTTCACAAAGTGAATTT 371  
 Db 410 AAAAGTACTCATATTCGAGGACCAAGTCTTCAAGTGAAGACAAATCGATTGGTAGCT 469  
 OY 372 GGGTCTTGAACATCTTAAGCTCAAGGCAAGGTTGAGTACTTGAAGAACAACAAGGA 431  
 Db 470 GGACTTTGGAGATCTTAAGCTCAAGGCGGAGCTTGAAGTTTACAGAAATTTATAGGC 529  
 OY 432 ATTTATGAGGAGATCTTGTATGCTTGAGCTTGAAGAGCTTCAAGCTTGGAGCATC 491  
 Db 530 ATTTATGAGGAGATCTTGTATGCTTGTAGCTTCAAGGAGCTTCAAAATTTGGAGCAGC 589  
 OY 492 AGCTGATGACAGCTATCAAGAGCATTAGGTCAAGAAAGCAACGATATTTGCAATCCA 551  
 Db 590 AACTGAGCTGCTCTTAAACACATAGATCGAAGAAAGATCAGCTCATGATGATCAATCA 649  
 OY 552 TATCTGCGCTCCAGAAAGAGATTAAGCCTTGCAAGATCACAACAATTCCTTCAAAA 611  
 Db 650 TCTCAGTCTTCAGAAAAAGATAGGCAATTCAGAGCAAAACAACCTGTTACAAAGGA 709  
 OY 612 AGATTAAGAGAGAGAAAGAAACGGGTGAGCAG 647  
 Db 710 AAGTAAGAGAGAGAGAGGAGCCTAGCGCAGCAAG 745

RESULT 8  
 AAT34431  
 ID AAT34431 standard; cDNA: 1070 BP.  
 AC AAT34431;  
 XX 01-OCR-1996 (first entry)  
 DT  
 XX Euca1yplus SOE2L cDNA.  
 DE  
 XX Euca1yplus; reproductive gene; SOE2L; Arabidopsis; agomous gene;  
 KW Antirrhinum; plena gene; sterility; fertility; forest tree;  
 KW transgenic plant; flower development; antisense; ribozyme; ss.  
 XX  
 OS Euca1yplus globulus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 184..921  
 FT /\*tag= a  
 FT /product= SOE-2L  
 XX  
 XX A09539013-A.  
 XX  
 XX 30-MAY-1996.  
 XX  
 XX 22-NOV-1995; 95AU-0039013.  
 XX  
 XX 22-NOV-1994; 94AU-0009589.  
 XX  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX  
 XX Dennis ES, Harcourt RL, Kyozeuka J, Llewellyn D;  
 PI Peacock WJ, Southern S;  
 XX  
 XX WPI: 1996-278411/29.  
 DR P-PSDB: AAR99636.  
 XX

PT Euca1yplus reproductive genes - useful for produ. of sterile  
 PT Euca1yplus trees useful for establishing wood lot plantations or in  
 PT re-forestation projects  
 PS Claim 8; Page 36-37; 60pp; English.  
 XX  
 CC cDNA clones SOE1 (AAT34429), SOE2S (AAT34430) and SOE2L (AAT34431) were  
 CC identified by homology to the MADS box of the Arabidopsis apetala  
 CC 1 (AP1) and Antirrhinum squamosa (SQUA) flower development genes.  
 CC They were obtd. by PCR amplification of E. globulus DNA using  
 CC primers based on the MADS box of the Arabidopsis and Antirrhinum  
 CC genes, followed by screening of a E. globulus young flower bud  
 CC library. The SOE2L cDNA codes for protein SOE2-L (AAR99636).  
 CC Antisense or ribozyme constructs of SOE or of FLE2 and SOE genes  
 CC (see also AAT34426, AAT34428 and AAT34432), may be used to produce  
 CC sterile transgenic Euca1yplus trees by minimising inflorescence.  
 XX  
 SQ Sequence 1070 BP; 308 A; 240 C; 270 G; 252 T; 0 other;

Query Match 29.3%; Score 311.2; DB 17; Length 1070;  
 Best Local Similarity 73.0%; Pred. No. 7.6e-70;  
 Matches 400; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

OY 99 ATATGGGAAGAGTGGGTTCACTGAGAGAGATAGAGAAACATATAGCAAGTTA 158  
 Db 182 AATGGGAGGGGAGGAGGTGAGAGAGATAGAGAAACATATAGCAAGTTA 241  
 OY 159 CTTTCTCAAGAAAGAGTGTGTTCTCAGAAAGCTCATGATCTCTGTCTCTGCG 218  
 Db 242 CTTTCTCAGAAAGAGTGTGTTCTCAGAAAGCTCATGATCTCTGTCTCTGCG 301  
 OY 219 ATGCTGAGGTTCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 278  
 Db 302 ACGCGGAGCTGCGCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 361  
 OY 279 ACTTTCATGAGAGAGATCTTGAACGCTATGATCTGATTTATATAGCAAAAC 338  
 Db 362 ACTGTTGATGAGAGAGATCTTGAACGCTATGATTTATATAGCAAAAC 421  
 OY 339 TTGTTGGCCGAGAGCTTTTCACAAAGTGAATTTGGGTTCTGAGACATGCTTAAGC 398  
 Db 422 TTCTCACAACCAATGCTCCGAAACCAATGGAACCTTGAACATGCAAAACCTCAAGG 481  
 OY 399 CAAGAGTTGAGTACTTGAAGAAACAAGAAATTTATGAGGGAAGATCTTGAATGCT 458  
 Db 482 CCAGATGAGAGATCTTGAAGAAACAAGAAATTTATGAGGGAAGATCTTGAATGCT 541  
 OY 459 TGAGCTTGAAGAGCTCCAAAGCTTGAAGAGATGATGATGATGATGATGATGATGAT 518  
 Db 542 TTAGCTTCAAGAGCTTCAAGATTTGAGAGATGATGATGATGATGATGATGATGATG 601  
 OY 519 GGTCAAGAAAGAACCAAGCTATGTTCAATTCATATCTGCGCTCAGAGAAAGATTAAG 578  
 Db 602 GGTCTAGAAAGATTCATCATCTGTAATTCATCTGAGCTTCAAGAAAGATTAAG 661  
 OY 579 CCTTGCATGATCAACAATTCGCTTCTCAAAAATTTAAGAGAGGAGAAAGAAAGG 638  
 Db 662 CGCTGCAAGAAACAAACAATCTGCGCAAAAGGTGAAGAGAGAGAGAGAGAGAGG 721  
 OY 639 GTGAGCAA 646  
 Db 722 CACAGCAA 729

RESULT 9  
 AAX17796  
 ID AAX17796 standard; cDNA to mRNA; 1131 BP.  
 AC AAX17796;  
 XX  
 XX 21-MAY-1999 (first entry)  
 DT  
 XX Petunia MADS box transcription factor, FBP10 encoding cDNA.  
 XX



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OY 101 ATGGAGAGAGTGGGTTGCTGAGCTGAAGAGATGAGAACAGATCAATAGCCAGTTACT 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ATGGAGAGGGGTAGGGTTCAGCTGACGTAAGAGGATGAGAACAGATCAACGCGAGTGCAG 60
OY 161 TTCTCAAGAGAGAGGCTGTTGGTCTCAAGAAAGCTCATGAGATCTGTCTCTGCGAT 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 TTTTCGAAGACGAAAGATGGGTGCTGTAAGAAAGGCGCATGAGATCTGTCTATGTCGAT 120
OY 221 GCTGAGGTTGCTCTCATGCTTCTCTCTCAAGAGCAAACTCTTGATATTCACCGAC 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 GCTCAGGTTGGCTTGTATGCTCTCTCTCAAGAGCAAACTCTTGATATTCACCGAT 180
OY 281 TCTTCATGAGAGAGATCTGAGCTGATGCTGATTTATATTCAGACAAACAGCT 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 TCATCATGAGAGATATCTGATGACGCTATGAGAGTACTGATGCGAGAGACAGCTA 240
OY 341 GTTGGCCGAGAGCTTTCAACAAAGTGAATGGGTTCTAGAACATGCTTAAGCTCAAGCA 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 GTGGAACCTAATTTGATTTCAACAGGGTAACCTGGCCCTTCGAACATGCTTAGGTTAAGTG 300
OY 401 AGAGTTGAGCTTCTGAGACAGAACAAAGAAATTTATGGGGGAAGATCTTGATTCGTTG 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 AAAGTTGAGCTTCTGAGACAGAACAAAGCTATTTGGGAGAGATCTGATTCATTTG 360
OY 461 AGCTTGAAGAGCTCCCAAGCTTGGAGCATCAGCTCGATGCGATCAAGAGCATTTAGG 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 361 AGTATCAAGAGATCCAAAGTTTGGAGCAAGCTTGAACCTGCTTTAAGCAAAATTTGCA 420
OY 521 TCAAGAAAGAACCAAGCTATGTTGCAATCCATATCTGCGCTCCAGAAAGATTAAGCC 580
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 421 TCAAGAAAGAACCAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 480
OY 581 TTGCAAGATCACACATTCGCTTCTCAAAAAGATTAAAGAGAGGAGAGAGAA 633
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 481 ATCAAGAGAGCAAGCAACTGCTTCAAAAAGATTAAAGAGAGGAGAGAGAA 533

RESULT 11
AAV58316
ID AAV58316 standard; DNA; 794 BP.
XX
AC AAV58316;
XX
DT 19-NOV-1998 (first entry)
XX
DE Brassica oleracea API gene.
XX
KW CAULIFLOWER gene; CAL gene; shoot meristem conversion; floral meristem;
    early flowering promotion; angiosperm; API gene; ds.
XX
OS Brassica oleracea.
XX
FH Key Location/Qualifiers
FT CDS 36..794
FT /*tag= a
XX
PN US5811536-A.
XX
PD 22-SEP-1998.
XX
PE 26-JAN-1996; 96US-0592214.
XX
PR 26-JAN-1996; 96US-0592214.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Yanofsky MF;
XX
DR WPI: 1998-530945/45.
XX P-PSDB: AAW69329.
XX
PT Cloned CAULIFLOWER genes - and vectors for converting shoot

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PT meristems to floral meristems
XX
PS Disclosure: Fig 2; 93pp; English.
XX
CC This sequence encodes the Brassica oleracea API protein. This sequence
CC was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER
CC (CAL) protein of the invention. An expression vector containing the CAL
CC DNA sequence can be used to convert shoot meristems to floral meristems,
CC especially to promote early flowering in angiosperms.
XX
SO Sequence 794 BP; 255 A; 171 C; 187 G; 181 T; 0 other;

Query Match      28.3%; Score 301; DB 19; Length 794;
Best Local Similarity 68.2%; Pred. No. 2.8e-67;
Matches 418; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

OY 85 TTGAAGAGAGAGATATGGAAGAGTATGGGTTGAGCTGAAGAGATGAGAACAGAT 144
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 TTTAAAGGATAAATGGAAGGATAGGTTGAGTGAAGAGATGAGAACAGAT 79
OY 145 CAATAGCGCACTTACTTTCTCAAGAGAAAGTGTGTTGCTCAAGAAAGCTCATGAGAT 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 CAATAGACAAAGTACATTTCTGAAAAAGAGAGCTGCTTATGAAAGAAAGCTCATGAGAT 139
OY 205 CTCTGTTCTGCGATGCTGAGTGTGCTCATGCTGCTCTCTTCCAAAGGCAACTCTT 264
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 140 CTCTGTTCTGTTGATGCTGGAAGTTGCGCTTGTGTTCTCTCCATAGGGAAACTCTT 199
OY 265 CGAATATTCACCGAAGCTTTGATGAGAGAGTACTTGAACGCTATGATCGCTATTTATA 324
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 200 TGAATATCTCACTGATTTCTGATGAGAAAGATCTGAAAGCTATGAGAGATCTCTTA 259
OY 325 TTCAACAACAACTTTGTTGGCCGAGAGCTTTCAACAAGTGAATTTGGGTTCTGAGACA 384
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 260 CGCCGAGAGACAGCTTATAGCACTGAGTCCGACTCCATACGACTGCTCATGAGAGTA 319
OY 385 TGCTAAGCTCAAGGCAAGGTGAGGTACTTGAGAAAGCAAAAGGAATTTATGGGGGA 444
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 320 TATATAGCTTATAGGCTTATAGATTGAGCTTTTGGAGAAACCAAGAGCACTATCTTGGGA 379
OY 445 AGATCTGATTCGTTGAGCTTGAAGAGCTCCAAAGCTTGAAGCATCAAGCTGATGCAAGC 504
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 380 AGACTTGAAGCAATGAGGCGCTTAAGGAACCTCCAGATCTAGAGCAACAGCTTGAATCTGC 439
OY 505 TATCAAGAGCATTTAGCTCAAGAAAGCAAGCTATGTTGCAATCTCATATCTGCGCTCCA 564
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 440 TCTTAAAGCAATCCGCTTAGAAGCAACCTATGTAAGCACTCATCAATCAAGACTCCA 499
OY 565 GAAGAAGGATTAAGGCTTGAAGATCACAACAATTCGCTTCAAAAAGATTAAAGAGAG 624
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 500 AAGAAAGGAGAAAGCCATACAGGAACAAACAGCATGCTTTCCAAAGCAGATTAAAGAGAG 559
OY 625 GGAGAAGAAAGGCTGAGCAAGAAAGCAATTAAGTCCAAATGCTCCAACTCTTCTTCAGT 684
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 560 GGAAGAAAGCTTTAGGCGCAACAGAGCAATGGGCGAGAGCAACCAATGAGGCAATTAAT 619
OY 685 TCTTCTGCTCA 697
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 620 GCCTCCGCTCCA 632

RESULT 12
AAT86629
ID AAT86629 standard; DNA; 794 BP.
XX
AC AAT86629;
XX
DT 18-JUN-1998 (first entry)
XX
DE APETALA1 gene from Brassica oleracea.
XX
KW Transgenic plant; ectopically expressed; meristem gene; APETALA1;
    API; CAULIFLOWER; CAL; LEAFY; LFY; reproductive development;

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KW		angiosperm, ds.	
OS		Brassica oleracea.	
XX			
XX	Key	Location/Qualifiers	
FH	CDS	36..794	
FT		/tag= a	
FT		/product= AP1-gene_product	
FT		/note= "No stop codon shown"	
XX			
PX		WO9746077-A1.	
PD		11-DEC-1997.	
XX			
PE		05-JUN-1996; 96WO-US09429.	
XX			
PR		05-JUN-1996; 96WO-US09429.	
XX			
PA		(REGC ) UNIV CALIFORNIA.	
PI		Weigel D, Yanofsky MF;	
DR		WPI; 1998-041769/04.	
DR		P-PSDB; AAW43110.	
XX			
PT		Transgenic plant comprising an ectopically expressed floral meristem gene - for promoting early reproductive development and controlling the time of seed-derived crop harvest(s) in e.g. grapes, beans, corn, wheat, etc	
XX			
PS		Disclosure; Pages 121-122; 158pp; English.	
XX			
CC		This sequence encodes a floral meristem identity gene product,	
CC		APETALA1 (API) from Brassica oleracea. The invention relates to	
CC		a non-naturally occurring seed plant comprising a first ectopically	
CC		expressible nucleic acid encoding a first floral meristem identity gene	
CC		product, provided that the first nucleic acid is not ectopically	
CC		expressed due to a mutation in an endogenous TERMINAL FLOWER gene.	
CC		The invention describes a method of converting shoot meristem to floral	
CC		meristem, especially in order to promote early reproductive development,	
CC		in an angiosperm, which comprises introducing a first ectopically	
CC		expressible nucleic acid molecule encoding a first floral meristem	
CC		identity gene product into the angiosperm. Ectopic expression of the	
CC		floral meristem gene product in the shoot meristem tissue of the	
CC		transgenic plant, allows selection of the time of seed development in	
CC		the plant which can be useful for manipulating the time of crop harvest	
CC		in seed-derived crops such as grapes, beans, corn, wheat, rice, hop,	
CC		etc., or to hasten the breeding of e.g. tree species, for insect or	
CC		disease resistance.	
XX			
SO		Sequence 794 BP; 255 A; 171 C; 187 G; 181 T; 0 other;	
	Query Match	28.3%; Score 301; DB 19; Length 794;	
	Best Local Similarity	68.2%; Pred. NO. 2.8e-67;	
	Matches 418; Conservative	0; Mismatches 195; Indels 0; Gaps 0;	
OY	85 TTGAAGACGACGATGTCGGAAAGCGTACGTCACTGGAAGAGCATGACACAAGAT	144	
Dd	20 TTTAAAGGGATAAAAATGGAAGGGGTGGGTTGAGTTGAAGAGCATGAAAAACAAGAT	79	
OY	145 CAATTGGGCAGTGACTTCTTCCAAGAAGAGGCTGGTTGGTCACAGAAGCTCATGAGAT	204	
Dd	80 CAATTGACACATGACATTTCTCGAAAAAAGAACGACGTGGCTTAATGAACAAAGCTCATGAGAT	139	
OY	205 CTCTGTTCTCTCCGATGCTGAGGTTGCTCTCATGCGCTCTCTCCCAAAGCAAACTCTT	264	
Dd	140 CTCGTCTCTGTTGATGCTGGAAGTTGCCGCTTGTGCTTCTCCCATTAAGGGCAAACTCTT	199	
OY	265 CGAATATTTCCACCGACCTGTGCATGAGAGATTAATTGAACGCTATGATCGCTATTATA	324	
Dd	200 TGAATATCTCACTGANTCTTGTATGAGAGAATACTTGAACGCTATGAGAATATCTCTTA	259	
OY	325 TTTCAGCAACAACACTGTGTTGGCCGAGACGTTTCACAAATGAAATTTGGGTTCTTAGACA	384	

Db		260	CGCCGAGACAGCTTTATAGCACCTGAGTCCGACTCCAAATTCGAACGTGGTGATGAGTA	319
Oy		385	TGCTTAGGCTCAAGGCAGAGTGTGAGGTACTTGGAGAACACAAAAGCAATTTTATGGGGGA	444
Dd		320	TAAATAGGCTTAAGGCTAAGATTGAGCTTTTGGAGAGAAACAGAGGACATATCTTGGGGA	379
Oy		445	AGATCTTGATTCGTTGAGCCTTGAAAGGAGCTCCAAAGCTTGGAGCATAGCTCGATGCAGC	504
Dd		380	AGACTTGCAGCAATAGACCCTTAAGGAACCTCACAATCTGAGGCMACAGCTTGATACTGC	439
Oy		505	TATCAAGGACATTAAGTACGAAGAAGAACCAAGCGATGTGTGAAATCCATATCTGCCGCCA	564
Dd		440	TTTTAGACATCTCCGCTTGAHAAAAACCACTTATGTAGCACTCCATCATGAGCTCCA	499
Oy		565	GAGAAGGATTAAGAGCTTGCACAAGATTCACMACAATTCCTCTCAAAGATTTAAGAGAG	624
Dd		500	AGGAAGGAGGAAGGCATACAGAAACAAACAGATGCTTTCCAAAGCATTTAAGGAGAG	559
Oy		625	GGAGAAGAAAAGGGGTGCGACAAGAGCAATTTGTGTCATGCTCCAACTCTTCTCAGT	684
Dd		560	GGAAAAACGTTCTTAAGGGCGCAACAAGACCAATGGGAGAGAGAACCATGGCCATATAT	619
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Dd		620	GCCTCCGCTTCCA	632
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ID	AAV02761			
XX	AAV02761 standard; cDNA; 794 BP.			
AC	AAV02761;			
XX				
DT	08-JUN-1998 (first entry)			
XX				
DE	Brassica oleracea floral meristem identity gene APETALA1 cDNA.			
KW	Floral meristem identity gene; APETALA1; API; transgenic plant;			
KW	angiosperm; seed development; ds.			
XX				
OS	Brassica oleracea.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	36..794		
FT		/*tag= a		
PX	WO9746078-A1.			
XX				
PD	11-DEC-1997.			
XX				
PP	05-JUN-1996; 96WO-US09453.			
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PR	05-JUN-1996; 96WO-US09453.			
PA	(REGC ) UNIV CALIFORNIA.			
XX				
PI	Yanofsky MF;			
XX				
DR	WPI: 1998-041770/04.			
DK	P-PsDB: AAM39132.			
XX				
PT	Nucleic acids encoding API floral meristem identity gene product			
PT	from cauliflower and maize - useful for promoting early reproductive			
PT	development and controlling the time of seed-derived crop harvest in			
PT	e.g. grapes, beans, corn, wheat, etc			
XX				
PS	Claim 2; Page 121-122; 156pp; English.			
CC	This sequence comprises Brassica oleracea APETALA1 (API) cDNA,			
CC	which encodes a floral meristem identity gene product (see AAM39132)			
CC	that is involved in the conversion of shoot meristem to floral			
CC	meristem. Mutation of the API gene results in replacement of basal			







GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2003, 23:33:46 ; Search time 59 Seconds  
(without alignments)  
5520.182 Million cell updates/sec

Title: US-09-981-087a-1

Perfect score: 1062  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1062	100.0	1062	4	US-09-067-800-1
2	1062	100.0	1062	4	US-09-105-652-1
3	1062	100.0	1062	4	US-09-349-677-1
4	301	28.3	794	1	US-08-592-214A-3
5	301	28.3	794	3	US-08-659-188-3
6	301	28.3	794	3	US-08-655-227-3
7	301	28.3	794	3	US-08-655-241-3
8	301	28.3	794	3	US-09-149-976-3
9	301	28.3	794	4	US-09-398-326-3
10	296.8	27.9	1054	2	US-08-576-156-1
11	296.8	27.9	1057	3	US-08-659-188-1
12	296.8	27.9	1057	3	US-08-655-227-1
13	296.8	27.9	1057	3	US-08-655-241-1
14	296.8	27.9	1057	3	US-09-398-326-1
15	296.8	27.9	1215	1	US-08-592-214A-1
16	296.8	27.9	1215	3	US-09-149-976-1
17	291.4	27.4	768	1	US-08-592-214A-5
18	291.4	27.4	768	3	US-08-659-188-5
19	291.4	27.4	768	3	US-08-655-227-5
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22	291.4	27.4	768	4	US-09-398-326-5
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25	266	25.0	779	3	US-08-655-227-9
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28	266	25.0	779	4	US-09-398-326-9	Sequence 9, Appli
29	255.8	24.1	1345	1	US-08-592-214A-7	Sequence 7, Appli
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31	255.8	24.1	1345	3	US-08-655-227-7	Sequence 7, Appli
32	255.8	24.1	1345	3	US-08-655-241-7	Sequence 7, Appli
33	255.8	24.1	1345	3	US-09-149-976-7	Sequence 7, Appli
34	255.8	24.1	1345	4	US-09-398-326-7	Sequence 7, Appli
35	252.6	23.8	756	1	US-08-592-214A-13	Sequence 13, Appli
36	252.6	23.8	756	3	US-08-659-188-13	Sequence 13, Appli
37	252.6	23.8	756	3	US-08-655-227-13	Sequence 13, Appli
38	252.6	23.8	756	3	US-08-655-241-13	Sequence 13, Appli
39	252.6	23.8	756	3	US-09-149-976-13	Sequence 13, Appli
40	252.6	23.8	756	4	US-09-398-326-13	Sequence 13, Appli
41	247.8	23.3	756	1	US-08-592-214A-11	Sequence 11, Appli
42	247.8	23.3	756	3	US-08-659-188-11	Sequence 11, Appli
43	247.8	23.3	756	3	US-08-655-227-11	Sequence 11, Appli
44	247.8	23.3	756	3	US-08-655-241-11	Sequence 11, Appli
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#### ALIGNMENTS

RESULT 1  
US-09-067-800-1  
; Sequence 1, Application US/09067800  
; Patent No. 6198024  
; GENERAL INFORMATION:  
; APPLICANT: Yanoitsky, Martin F.  
; APPLICANT: Ferrandiz, Cristina  
; TITLE OF INVENTION: Seed Plants Characterized by Delayed  
; TITLE OF INVENTION: Seed Dispersal  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESSES:  
; ADDRESS: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/067,800  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 2948  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1062 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 101..827  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1062  
; OTHER INFORMATION: /note= "There is a poly(A) tail at  
; FEATURE:  
; NAME/KEY: misc\_feature

LOCATION: 1..1062  
OTHER INFORMATION: /note="Nucleotide and Deduced  
OTHER INFORMATION: Amino Acid Sequences of the Aql8 cDNA clone."  
US-09-067-800-1

Query Match 100.0%; Score 1062; DB 4; Length 1062;  
Best Local Similarity 100.0%; Pred. No. 1.4e-299;  
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CCCAGAGAGCATAGAGAGAGAGAGAGAGATCTTGGTCATTTGAGGCTTCG 60
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## RESULT 2

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US-09-105-652-1
; Sequence 1, Application US/09105652
; Patent No. 6229068
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Marienssen, Robert
; APPLICANT: Ferrandiz, Cristina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/105,652
; EARLIER FILING DATE: 1998-06-26
; EARLIER APPLICATION NUMBER: 60/051,030
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(826)
; FEATURE:
; NAME/KEY: polyA-signal
; LOCATION: (1061)
US-09-105-652-1
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Query Match 100.0%; Score 1062; DB 4; Length 1062;  
Best Local Similarity 100.0%; Pred. No. 1.4e-299;  
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120
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RESULT 3  
US-09-349-677-1  
: Sequence 1, Application US/09349677  
: Patent No. 6288305  
: GENERAL INFORMATION:  
: APPLICANT: Yanofsky, Martin F.  
: APPLICANT: Ferrandiz, Cristina  
: TITLE OF INVENTION: Seed Plants Characterized by Delayed  
: TITLE OF INVENTION: Seed Dispersal  
: NUMBER OF SEQUENCES: 24  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Campbell & Flores LLP  
: STREET: 4370 La Jolla Village Drive, Suite 700  
: CITY: San Diego  
: STATE: California  
: COUNTRY: United States  
: ZIP: 92122  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/349,677  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 09/067,800  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 2948  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1062 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 101..827  
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NAME/KEY: misc\_feature  
LOCATION: 1062  
OTHER INFORMATION: /note= "There is a poly(A) tail at  
OTHER INFORMATION: the end."  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..1062  
OTHER INFORMATION: /note= "Nucleotide and Deduced  
OTHER INFORMATION: Amino Acid Sequences of the AGL8 cDNA clone."  
US-09-349-677-1

Query Match 100.0%; Score 1062; DB 4; Length 1062;  
Best Local Similarity 100.0%; Pred. No. 1,4e-299;  
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCAGAGACATTAAGAAAGAGAGAGAGATCTTTGGTCAATTCACGGTTGTG 60  
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## RESULT 4

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US-08-592-214A-3
; Sequence 3, Application US/08592214A
; Patent No. 5811536

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## GENERAL INFORMATION:

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APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536

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## ATTORNEY/AGENT INFORMATION:

```

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

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## INFORMATION FOR SEQ ID NO: 3:

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SEQUENCE CHARACTERISTICS:
LENGTH: 794 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 36..794

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..794
; OTHER INFORMATION: /note="product = Brassica oleracea"
; OTHER INFORMATION: API"
US-08-592-214A-3

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Query Match      28.3%; Score 301; DB 1; Length 794;
Best Local Similarity 68.2%; Pred. No. 4,2e-78;
Matches 418; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

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Oy 85 TTGAAGAGAGAGATATAGGAGAGAGAGGTTGCTGCTGAGAGATATAGAGACAGAT 144
Db 20 TTTAAAGAGGATATAAATAGGAGAGGTTGCTGCTGAGAGATATAGAGACAGAT 79
Oy 145 CAATGAGGAGATCTTCTTCAAGAGAGGTTGCTGCTGAGAGATATAGAGACAGAT 204
Db 80 CAATGAGGAGATCTTCTTCAAGAGAGGTTGCTGCTGAGAGATATAGAGACAGAT 139
Oy 205 CTTCTGTTCTGCGATGCTGAGGTTGCTGCTGATCGTCTTCTTCAAGAGGAACTCTT 264
Db 140 CTTCTGTTCTGTTGATGCTGAGGTTGCTGCTGATCGTCTTCTTCAAGAGGAACTCTT 199
Oy 265 CGAATATCTCAGGACTTTCATGAGAGATCTTGAAGGATATGATGCTATATATA 324
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Oy 325 TTGAGCAAAACAATGTTGGCGGAGAGCTTTCACAAAGTGAAGAAATGGGTTCTGAGACA 384
Db 260 CGCGAGAGAGAGCTTATAGACCTGATGACCTGATGACCTGATGACCTGATGAGTA 319
Oy 385 TGCTAAGCTTCAAGCAAGATGAGTACTTGAGAGAGAGAGAGAGATATATATATAT 444
Db 320 TATATAGCTTAAAGCTTAAAGTATGAGCTTTTGGAGAGAGAGAGAGAGAGATATAT 379
Oy 445 AGATCTTGATGCTTGAAGCTTGAAGAGCTCCAAAGCTTGAAGATGATGATGAGC 504
Db 380 AGACTTGAAGCAATGAGCTTGAAGAGCTCCAAAGCTTGAAGATGATGATGAGC 439
Oy 505 TATCAAGAGCTATGATGCAAGAGAGAGAGAGAGAGATGATGATGATGATGATGAT 564
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Oy 565 GAAGAAGATTAAGCCTTCAAGATCAACAATTCGTTCTCAAAAGAGATTAGAGAG 624
Db 500 AAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 559
Oy 625 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 684
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Oy 685 TCTTCTGCTCA 697
Db 620 GCTTCTGCTCA 632

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## RESULT 5

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US-08-659-188-3
; Sequence 3, Application US/08659188
; Patent No. 6002069

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## GENERAL INFORMATION:

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APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

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COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/659,188  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1946  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 794 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 36..794  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 1..794  
OTHER INFORMATION: /note= "product = Brassica oleracea  
OTHER INFORMATION: APl."  
US-08-659-188-3

Query Match 28.3%; Score 301; DB 3; Length 794;  
Best Local Similarity 68.2%; Pred. No. 4.2e-78;

Matches 418; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

85 TTGAAGAGAGAGATATGCGAAGAGTATGAGTTCAGTGAAGAGATAGAGACAAGAT 144  
20 TTTAAAGGATATAAATGGGAAGGGTATGAGTTGAGTGAAGAGATGAAACAGAT 79  
145 CAATAGGCAAGTACTTCTTCAAGAGAAAGCTGCTGCTCAAGAAAGCTCATGAGAT 204  
80 CAATAGACAAGTATCTCGAAAAGAGACCTGCTTATGAAAGAAAGCTCATGAGAT 139  
205 CTCTGTTCTGCGATGCGAGAGTTCATGCTCATGCTCTTCCAAAGGAACTCTT 264  
140 CTCTGTTCTGCTGATGCTGAAGTTGCGCTTGTCTTCTCCATAGGGGAACTCTT 199  
265 CGAATATTCACCGACTTTCATGAGAGATGATGAAACGCTATGATGCTATTATTA 324  
200 TCAATATCTCCACTGATTTCTTATGAGAGAGATGATGAAAGCTATGAGATGATCTTA 259  
325 TTCAAGACAAGCTGTTGGCCGAGAGCTTTCACAAAGTGAATTTGGGTTCTAGACA 384  
260 CGCCGAGAGACGCTTATGACACCTGAGTCCGACTCCATATGAACTGGTCGATGAGTA 319  
385 TGCTAGCTCAAGGCAAGGTTAGGTACTCTTGAAGAAACAAGAAATTTATGGGGA 444  
320 TAAATAGGCTTAAGGCTTAAGATTTGAGAGAAACCGAGGCACTATCTTGGGGA 379  
445 AGATCTTGAATCGTTGAGCTTGAAGAGCTCCAAAGCTTGAAGCTCAAGCTGATGAGC 504  
380 AGACTTGAAGCAATGAGGCCCTAAGAACTCCAGATCTAGAGCAACAGCTTGAATCTGC 439  
505 TATCAAGACATTTAGCTCAAGAAACAAGCTTATGTTGCAATCCATATCTGCGCTCA 564  
440 TCTTAAAGCAATCCGCTCAGAAAACCACTTATGTAAGCACTCATTCAATGAGACTCA 499  
565 GAAGAAGATTAAGCTTGAAGATCAACAATTCGCTTCCAAAAGATTAAAGAGAG 624  
500 AAGAAAGGAGAAAGCCATTAACAGAAACAAGCAATGCTTTTCAAGCAATTAAGGAGAG 559  
625 GGAGAAGAAAAGGGTCAAGCAAGAAAGCAATTTAGTCCAAATGCTCAACTCTTCTTCA 684

Db 560 GGAAGAGCTTCTTAGGCGCAACAGACGAGAGCAAGACCATAGGCATATATAT 619  
QY 685 TCTTCTGCTCA 697  
Db 620 GCCTCGCCTCA 632

RESULT 6

US-08-655-227-3  
Sequence 3, Application US/08655227  
Patent No. 6025483

GENERAL INFORMATION:  
Applicant: Yanofsky, Martin F.

TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene  
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same  
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego

STATE: California  
COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/655,227  
FILING DATE: 05-JUN-1996

CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 2143  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 794 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
FEATURE:

NAME/KEY: CDS  
LOCATION: 36..794

FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 1..794

OTHER INFORMATION: /note= "product = Brassica oleracea  
OTHER INFORMATION: APl."  
US-08-655-227-3

Query Match 28.3%; Score 301; DB 3; Length 794;  
Best Local Similarity 68.2%; Pred. No. 4.2e-78;

Matches 418; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

85 TTGAAGAGAGAGATATGCGAAGAGTATGAGTTCAGTGAAGAGATAGAGACAAGAT 144  
20 TTTAAAGGATATAAATGGGAAGGGTATGAGTTGAGTGAAGAGATGAAACAGAT 79  
145 CAATAGGCAAGTACTTCTTCAAGAGAAAGCTGCTGCTCAAGAAAGCTCATGAGAT 204  
80 CAATAGACAAGTATCTCGAAAAGAGACCTGCTTATGAAAGAAAGCTCATGAGAT 139  
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140 CTCTGTTCTGCTGATGCTGAAGTTGCGCTTGTCTTCTTCTTCCATTAAGGGGAACTCTT 199

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OY 265 CGAATATTCACCGACTTTGATGAGAGAGATCTGAAACGCTGATGCTATTATTATA 324
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DB 200 TGAATACCTCAGTATTTGATGAGAGAGATCTGAAACGCTGATGAGATCTCTTA 259
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OY 325 TTCAGCAAAACACTGTTGGCCGAGACGTTTCAAAAGGAAATGGGTTCTAGACACA 384
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DB 260 CGCGGAGAACACCTTATAGCACCCTGAGTCCGACTCCAAATACGAACTGGTCGATGAGTA 319
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OY 385 TGTCTAGCTCAAGGCAAGATTGAGTACTTGTAGAGAGAGAAAGAAATTTTATGGGGA 444
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DB 320 TATAGGCTTAAGGCTAAGATTGAGCTTTTGGAGAGAGAACAGAGACATCTTGGGGA 379
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OY 445 AGATCTGATTCGTTGAGCTTGAAGAGCTCCAAAGCTTGAGAGATGCTGATGAGC 504
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DB 440 TCTTAAGCAATCCGCTTGAAGAAAAAACCACTTATGTAGCACTCCATCAATGAGCTCCA 499
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OY 625 GGAGAAAGAAAGCGGTGACAGAGAGACATTAATGCTCAATGCTTCTTCAGT 684
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DB 560 GGAAGAAAGCTTCTTAAGGCGGACACAGAGCAATGAGAGAGACAGACATGCGCATATAT 619
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DB 620 GCCTCGCTCCA 632
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## RESULT 7

US-08-655-241-3

; Sequence 3, Application US/08655241

; Patent No. 6025543

; GENERAL INFORMATION:

; APPLICANT: Yanoofsky, Martin F.

; APPLICANT: Weigel, Detlef

; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive

; TITLE OF INVENTION: Development and Methods of Making Same

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell and Flores

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentia Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/655,241

; FILING DATE: 05-JUN-1996

; CLASSIFICATION: CLASS 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathlyn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-UD 1894

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 794 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36..794
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..794
; OTHER INFORMATION: /note="product = Brassica oleracea
; OTHER INFORMATION: APL."
; US-08-655-241-3

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## Query Match

28.3%; Score 301; DB 3; Length 794;

Best Local Similarity 68.2%; Pred. No. 4,2e-78;

Matches 418; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

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DB 80 CAATAGCAAGTACATCTTCGAAAGAGAGCTGGCTTATGAAGAAAGCTCATGAGAT 139
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OY 205 CTCTGTTCTGCGATGCTGAGGTTGCTCATGCTTCTCTTCAAAAGCAAACTCTT 264
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DB 140 CTCTGTTCTGTTGATGCTGAAGTTGCGCTTGTCTTCTCCATTAAGGGAACTCTT 199
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OY 265 CGAATATTCACCGACTTGTGATGAGAGAGATCTGAAGCTTGAATCGCTATTTATA 324
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DB 200 TGAATACCTCAGTATTTGATGAGAGAGATCTGAAGCTTGAATCGCTATTTATA 259
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DB 260 CGCGGAGAGACAGCTTATAGCACCCTGAGTCCGACTCCAAATGAGACATGCTGATGAGTA 319
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DB 320 TATAGGCTTAAGGCTAAGATTGAGCTTTTGGAGAGAAACGAGCAATATCTTGGGGA 379
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DB 380 AGACTTGCAAGCAATGAGCGGCTTGAAGAGAGCTCCAGATCTAAGAGCAATGATACCTTA 439
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DB 440 TCTTAAGCAATCCGCTTGAAGAAAAACCACTTATGAGAGCTCAGTCATCAATGAGACTCCA 499
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OY 565 GAAGAGAGATTAAGCTTGCAGATGCAACAATTCGCTTCAAAAAGATTAAAGAGAG 624
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DB 500 AAGAAAGAGAAAGCCATACAGAGACAAAGACATGCTTTCAGAGATTAAGAGAG 559
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OY 625 GGAGAAAGAAAGCGGTGACAGAGAGACAAATTAATGCTCAACTCTTCTTCAGT 684
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DB 560 GGAAGAAAGCTTCTTAAGGCGGACACAGAGCAATGAGAGAGAGCAATGGCATATAT 619
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OY 685 TCTTTCGCTCA 697
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DB 620 GCCTCGCTCCA 632
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## RESULT 8

US-09-149-976-3

; Sequence 3, Application US/09149976

; Patent No. 6127123

; GENERAL INFORMATION:

; APPLICANT: Yanoofsky, Martin F.

; TITLE OF INVENTION: Cauliflower Floral Meristem Identity

; TITLE OF INVENTION: Genes and Methods of Using Same

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell &amp; Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California





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0Y      145  CAAATAGGCAAGTACTTCTCTCAAAAGAGAGGCTGGTTTGCTCAAGAAAGCTCATGAGAT 204
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0Y      265  GCAATATTCACCCGACTCTTGATATGAGAGATACTTGAACGCTATGATGCTATTTATA 324
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Db      200  TGAATATCTCATGATTTCTTGATGGAAGATATCTTGAAACGCTATGAGATATCTCTTA 259
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0Y      325  TTCAGACAACCACTTGTGTGGCCGAGAGCTTTCACAAAGTGAATAATTGGCTTAGAACA 384
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Db      260  GCCCGAGAGACGCTTATATAGACCTCGACTCCGACTCCCAATACGAACGTGTCGATGAGAGTA 319
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0Y      385  TCTCTAAGCTCAAGGCAAGAGTTGAGCTACTTGAGAGAACAAAGAAATTTTATGGGGGA 444
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Db      320  TATATGCGCTTAAGGCTAAGATTTGACCTTTTGGAGAGAAACGAGGACACTATCTTGGGGGA 379
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0Y      445  ACATCTGTGTTGCTTGAGCTTGAAGGACTCTCAAAAGCTTGAGAGATGAGCTCATGAGC 504
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Db      380  ACACCTTGCAAGCAATGAGCCTTAAGAGACTCAGATCTAGAGAACACGCTTGATATGTC 439
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0Y      505  TATCAAGACATTAAGTCAAGAAAGAACCAAGCATGTCTTCAATCTCATCTATCTGGGCTCA 564
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Db      440  TCTTAAGCAATCCGCTCTAGAAAAAACCAACTATATGACACCTCATCAATGAGCTCCA 499
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0Y      565  GAGAAGAGTAAAGCTTGCAGATCACACAATTCGCTCTCAAAAAGATTAAAGAGAG 624
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0Y      685  TCTTCTGCCTCAA 697
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Db      620  GCCTCCGCTCCA 632
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RESULT 10
US-08-576-156-1
: Sequence 1, Application US/08576156
: Patent No. 5844119
: GENERAL INFORMATION:
: APPLICANT: Weigel, Detlef
: TITLE OF INVENTION: Genetically Modified Plants Having Modulated
: TITLE OF INVENTION: Flower Development
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: US
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows95
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/576,156
: FILING DATE: 12-21-95
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/360,336
: FILING DATE: 12-21-94
: ATTORNEY/AGENT INFORMATION:
: NAME: Hallie, Lisa A.
: REGISTRATION NUMBER: 38,347

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:	REFERENCE//DOCKET NUMBER:	07251/013001
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE:	619-678-5070
:	TELEFAX:	619-678-5099
:	INFORMATION FOR SEQ ID NO:	1:
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH:	1054
:	TYPE:	nucleic acid
:	STRANDEDNESS:	single
:	TOPOLOGY:	linear
:	US-08-576-156-1	
Query Match	27.9%;	Score 296.8; DB 2; Length 1054;
Best Local Similarity	69.5%;	Pred. No. 8e-77;
Matches 403; Conservative	0;	Mismatches 177; Indels 0; Gaps 0
Qy	84	TTTGAGAGAGAGATATGGGAGGTAGGGCTTCACCTGAAGAAGATAGACAACA 143
Db	107	TTAAATAAGCATCAAAAATTGGGAAGGGGTAGGGTTCATATGAAGGATAGACAACA 166
Qy	144	TGCATAGGCAAGTACTTCTCATAAAGAAGGTCTGGTTGCTCAGAAGAGCTCATAGA 203
Db	167	TCAATBACACAGGACATCTCCAAAAAGAGCGTGCTTTTGAAAGAACCTCATAGA 226
Qy	204	TCTGTGTTCTCTCGAATGCTGAGGTGGCTCATCGTCTTCTTCCAAGAGCAAACCT 263
Db	227	TCTGTGTTCTCTGATGCTGAAGTTGGCTCTTGTCTTCTCCCATRAGGGAACTCT 286
Qy	264	TGCAATATTCACCACGACTCTTGATGAGAGAGATCTTGAACGCTATGATCGATTAT 323
Db	287	TGCAATACTCCACTGATTTCTTGATGAGAGATGATCTTGAACGCTATGAGAGGACT 346
Qy	324	ATTTAGCAACAACACTGTTGGGCCGAGACGTTTCACAAAGTGAAAAATTGGCTCTGA 383
Db	347	ACGGCGAAACACGCTTATTGCACTGAGTCGACGTCATTAACCAACTGGTGCATGAG 406
Qy	384	ATGCTAGCTCAAGCAGAGAGTTGAGGTACTTGAGACAGAACAAAAGAAATTTATGGGG 443
Db	407	ATACAGGCTTAAAGCTTAAGATTGACCTTTTGGAGAGAAACCAAGGCACTTATCTTGGGG 466
Qy	444	AAGATCTTGATTTGGTGGACTTGAAGAGAGCTTCAAGGCTTGAGACATCAGCTGATGAC 503
Db	467	AAGACTTGCAGGAATAGAGCCCTCAAGAGGCTTCAAGAAATCTGGACACAGCTTGACACT 526
Qy	504	CTATCAGAGCAATTAGGTCAAGAAAGAACCAAGCTATGTTGAAATCCATATCTGCGCTCC 563
Db	527	CTCTTAAGCAATCCACACTAGAAAAAACCACTTATGTACAGCTCATCAATGAGCTCC 586
Qy	564	AGAAAGAGGTAATAGGCTTGCAGAAATCACAAATTCCTCTCAAAAAGCTTAAAGAGAG 623
Db	587	AAAAAAGGAGAGGCGCATATCAGAGACAAACAGCATCTTCTTAAACAGATCAAGAGAG 646
Qy	624	GCGAGAGAAAAAGGCTCAGCAAGAGACATTAATAGTCCA 663
Db	647	GCGAAAAAATTTTAGGGCTCAACAGAGACAGTGGGATCA 686
RESULT 11		
US-08-659-188-1		
Sequence 1, Application US/08659188		
Patent No. 6002069		
GENERAL INFORMATION:		
APPLICANT:	Yanofsky, Martin F.	
TITLE OF INVENTION:	seed Plants Exhibiting Inducible Early	
TITLE OF INVENTION:	Reproductive Development and Methods of Making Same	
NUMBER OF SEQUENCES:	26	
CORRESPONDENCE ADDRESS:		
ADDRESSEE:	Campbell and Flores	
STREET:	4370 La Jolla Village Drive, Suite 700	
CITY:	San Diego	
STATE:	California	
COUNTRY:	USA	
ZIP:	92122	

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/659,188  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1946  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1057 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 124..893  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..1057  
OTHER INFORMATION: /note= "product = Arabidopsis  
OTHER INFORMATION: thaliana Apl."  
US-08-659-188-1

Query Match 27.9%; Score 296.8; DB 3; Length 1057;  
Best Local Similarity 69.5%; Pred. No. 8e-77;  
Matches 403; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

84 TTTGAGAGAGAGATATGAGAGAGTACAGCTCAAGAGATAGAGACAAGA 143  
107 TTTAAAAAGATCAAAAATGGGAAGGGTTCATTTGAGAGATAGAGACAAGA 166  
144 TCAATAGCAAGTACTTTCTCAAGAGAGGTTGCTTCAAGAAAGCTCATAGA 203  
167 TCAATAGCAAGTACTTTCTCAAGAGAGGTTGCTTCAAGAAAGCTCATAGA 226  
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227 TCTGTTCTCTGAGATGAGTGTGCTCTCTCTCTTCCAAAGCAACTCT 286  
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287 TCGAATATTCACCGACTTTCATGAGAGAGATCTTGAACGCTATGAGAGTACTCT 346  
324 ATTCAAGACAACACTTGTGGCGGAGAGCTTTCACAAAGTGAAATTTGGTTTCAAGAC 383  
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564 AGAAGAGGATTAAGCTTGAAGAGAAACCAAGCTATGCTTCAATCTGCGCTCC 623  
587 AAAAAAGAGAGAGCCATCAGAGAGCAAAACGATGCTTTCTTAAAGATCAAGAGAGA 646  
624 GGGAGAGAAAAAGGCTGAGCAAGAGAGCAATTAAGTCCA 663

DB 647 GGGAAAAAATCTTAGGGCTCAACAGGACAGTGGGATCA 686

RESULT 12  
US-08-655-227-1

; Sequence 1, Application US/08655227  
; Patent No. 6025483

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

; TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene

; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell and Flores

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/655,227

FILING DATE: 05-JUN-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 2143

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1057 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 124..893

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..1057

OTHER INFORMATION: /note= "product = Arabidopsis

OTHER INFORMATION: thaliana Apl."

US-08-655-227-1

Query Match 27.9%; Score 296.8; DB 3; Length 1057;  
Best Local Similarity 69.5%; Pred. No. 8e-77;  
Matches 403; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

84 TTTGAGAGAGAGATATGAGAGAGTACAGCTCAAGAGATAGAGACAAGA 143  
107 TTTAAAAAGATCAAAAATGGGAAGGGTTCATTTGAGAGATAGAGACAAGA 166  
144 TCAATAGCAAGTACTTTCTCAAGAGAGGTTGCTTCAAGAAAGCTCATAGA 203  
167 TCAATAGCAAGTACTTTCTCAAGAGAGGTTGCTTCAAGAAAGCTCATAGA 226  
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QY 444 AAGATCTTATTCGTTGAGGCTTGAAGAGCTCCAAAGCTTGGAGCATCAGCTGATG 503  
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Db 647 GGGAAAAAATTTCTTAGGCTCAACAGAGAGAGTGGATCA 686

## RESULT 13

US-08-655-241-1  
: Sequence 1, Application US/08655241  
: Patent No. 6025543

## GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.  
APPLICANT: Weigel, Detlef  
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive  
TITLE OF INVENTION: Development and Methods of Making Same  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/655,241  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: CLASS 800

## ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1894  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1057 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

## FEATURE:

NAME/KEY: CDS  
LOCATION: 124..893

## FEATURE:

NAME/KEY: misc\_feature  
LOCATION: 1..1057  
OTHER INFORMATION: /note= "product - Arabidopsis  
OTHER INFORMATION: thaliana Apl."  
US-08-655-241-1

Query Match 27.9%; Score 296.8; DB 3; Length 1057;  
Best Local Similarity 69.5%; Pred. No. 8e-77;  
Matches 403; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 84 TTGAAGAGAGAGATATGAGAGAGTGGTTCAGCTGAAGAGATAGAGAACAGA 143  
Db 107 TTAAGAAAGGATCAAAAATGGAAGGCTAAGGCTTCAATTTGAAGAGATAGAGAACAGA 166  
QY 144 TCAATAGGCAAGTACTTCTCAAGAGAGGCTGTTTGCACAAAGCTCATGAGA 203  
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QY 204 TCTCTGTTCTCTCGATGAGTGTCTCATCTCTCTCTCTCTCTCTCTCTCTCT 263  
Db 227 TCTCTGTTCTCTGATGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 286  
QY 264 TCGAATATTCACCGAGCTCTGATGAGAGATCTTGAAGAGATCTTGAAGAGATCT 323  
Db 287 TCGAATATTCACCGAGCTCTGATGAGAGATCTTGAAGAGATCTTGAAGAGATCT 346  
QY 324 ATTACAGCAACAACTTGTGCGGAGAGCTTTCACAAAGTGAAATTTGGTTAGAAC 383  
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QY 384 ATGCTAAGCTCAAGGCAAGGCTTACTTGAAGAGCAAAAGCAATTTATGGGG 443  
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## RESULT 14

US-09-398-326-1  
: Sequence 1, Application US/09398326  
: Patent No. 6355863

## GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early  
TITLE OF INVENTION: Reproductive Development and Methods of Making Same  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/398,326  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/659,188  
FILING DATE: 05-JUN-1996



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QY 564 AGAAGAGGATTAAGCCTTGCAAGATCAGACAAATTCGCTCTCAAAAAAGATTAAAGAGA 623
Db 604 AAAAAAGGAGAGGCGCATATACAGAGCAAAACAGCATGCTTCTTCTAAACAGATCAAGGAGA 663
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Search completed: February 2, 2003, 05:34:26  
 Job time : 64 secs



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Db	1021	AGAACAAAGATTCATCTTGGTATGATTTCTCATGAATA	1062
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US-09-981-087A-1			
; Sequence 1, Application US/09981087A			
; Patent No. US20020178466A1			
; GENERAL INFORMATION:			
; APPLICANT: Yanofsky, Martin F.			
; APPLICANT: Liljegen, Sarah			
; APPLICANT: Fairchildz, Cristina			
APPLICANT: The Regents of the University of California			

	:	TITLE OF INVENTION:	Selective Control of Lipid Biosynthesis in Transgenic
	:	: TITLE OF INVENTION:	Plants
	:	: FILE REFERENCE:	19452A-000940US
	:	: CURRENT APPLICATION NUMBER:	US/09/981,087A
	:	: CURRENT FILING DATE:	2002-05-21
	:	: PRIOR APPLICATION NUMBER:	US 60/090,649
	:	: PRIOR FILING DATE:	1998-06-25
	:	: PRIOR APPLICATION NUMBER:	US 09/339,998
	:	: PRIOR FILING DATE:	1999-06-25
	:	: NUMBER OF SEQ ID NOS:	25
	:	: SOFTWARE:	Patentlin Ver. 2.1
	:	: SEQ ID NO 1	
	:	: LENGTH:	1062
	:	: TYPE:	DNA
	:	: ORGANISM:	Arabidopsis sp.
	:	: FEATURE:	
	:	: NAME/KEY:	CDS
	:	: LOCATION:	(101)..(829)
	:	: OTHER INFORMATION:	AGAMOUS-LIKE 8 (AGL8)
	:	: US-09-981-087A-1	
Query Match:		100.0%;	Score 1062; DB 9; Length 1062;
Best Local Similarity:		100.0%;	Pred. No. 1.2e+26;
Matches 1062;		Conservative	0; Mismatches 0; Indels 0; Gaps 0
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Oy		361	AAGTGAAGAAATGGGTTCTTAGAACATGCTTAACCTCAAGCAAGATTGAGTACTTGAAGA
Dd		361	AAGTGAAGAAATGGGTTCTTAGAACATGCTTAACCTCAAGCAAGATTGAGTACTTGAAGA
Oy		421	GAAACAAAGAAATTTATGGGGGAAGATCTTGATTCGTTGAGCTTGAAGAGCTCCAAAG
Dd		421	GAAACAAAGAAATTTATGGGGGAAGATCTTGATTCGTTGAGCTTGAAGAGCTCCAAAG
Oy		481	CTTGGACATCACGCTGATGACGCTATCAGACATTTAGGTCAGAAAGAACCAAGCTAT
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Oy		541	GTTTCGAATCATATTCGGGCTCCGAAGAAAGATTAAGCCCTTGCAAGATACAAACATTC
Dd		541	GTTTCGAATCATATTCGGGCTCCGAAGAAAGATTAAGCCCTTGCAAGATACAAACATTC
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Dd		601	GCTTTCAAAAAGATTAAAGAGAGGAGAAACAAAGCGGTACGACAAAGAAAGCAATTACT
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## RESULT 3

US-09-978-382A-1

; Sequence 1, Application US/09978382A  
; Publication No. US20020194647A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegren, Sarah  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000930US  
; CURRENT APPLICATION NUMBER: US/09/978, 382A  
; PRIOR FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/090, 649  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: US 09/339, 998  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1062  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(829)  
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)  
; US-09-978-382A-1

Query Match 100.0%; Score 1062; DB 9; Length 1062;

Best Local Similarity 100.0%; Pred. No. 1.2e-266;

Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 GAAACAAAGGATTTTATGAGGAGAGATCTTATCTGATCTGAGTCAAGGACTCCAAAG 480  
QY 481 CTTGAGACATCAGCTCGATGAGCTATCAAGAGCAATTAGTCAAGAAAGCAAGCTAT 540  
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Db 481 CTTGAGACATCAGCTCGATGAGCTATCAAGAGCAATTAGTCAAGAAAGCAAGCTAT 540  
QY 541 GTTCGAATCCATATCTGCGCTCCAGAGAGAGATTAAGCCTTGCAAGATCACAACATTC 600  
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| | | | |  
Db 601 GCTTCTCAAAAAGATTAAAGAGAGAGAGAGAAACGGCTCAGCAAGAGAGCAATTA 660  
QY 661 CCAATGCTCCAACTCTTCTCAGTCTTCTGCTCAATCTGCTGATCTGCTCCAGAGA 720  
| | | | |  
Db 661 CCAATGCTCCAACTCTTCTCAGTCTTCTGCTCAATCTGCTGATCTGCTCCAGAGA 720  
QY 721 TGGCTTTGGAGAGAGTTGGGGGAGAGACGCGTGTGATCGTCTGACGAGCAACAAA 780  
| | | | |  
Db 721 TGGCTTTGGAGAGAGTTGGGGGAGAGACGCGTGTGATCGTCTGACGAGCAACAAA 780  
QY 781 CTCCTGCTTCGGCGCTTGAGTGTACGTCCTACACCTACGAGAGAGTGAACATCTCAC 840  
| | | | |  
Db 781 CTCCTGCTTCGGCGCTTGAGTGTACGTCCTACACCTACGAGAGAGTGAACATCTCAC 840  
QY 841 TCTTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 900  
| | | | |  
Db 841 TCTTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 900  
QY 901 TTTGGTGAATATATATATATATATATATATATATATATATATATATATATATATATAT 960  
| | | | |  
Db 901 TTTGGTGAATATATATATATATATATATATATATATATATATATATATATATATATAT 960  
QY 961 GATGGAACCTCGTGTGAGAGAGATATATATATATATATATATATATATATATATATAT 1020  
| | | | |  
Db 961 GATGGAACCTCGTGTGAGAGAGATATATATATATATATATATATATATATATATATAT 1020  
QY 1021 AGAACAAAGATTATATATATATATATATATATATATATATATATATATATATATAT 1062  
| | | | |  
Db 1021 AGAACAAAGATTATATATATATATATATATATATATATATATATATATATATATAT 1062

## RESULT 4

US-09-978-740A-1

; Sequence 1, Application US/09978740A  
; Publication No. US20030005481A1  
; GENERAL INFORMATION:  
; APPLICANT: Yanofsky, Martin F.  
; APPLICANT: Liljegren, Sarah  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 19452A-000960US  
; CURRENT APPLICATION NUMBER: US/09/978, 740A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/090, 649  
; PRIOR FILING DATE: 1998-06-25



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Db 301 TGAACGCTATGATCGCTATTATATTCACAGCAAAACACTTTGGCCGAGACCTTCACA 360
Qy 361 AAGTGAATTTGGTTCTGAACATGCTAAGCTCAAGGCAAGAGTTGAGTACTTGAGAA 420
Db 361 AAGTGAATTTGGTTCTGAACATGCTAAGCTCAAGGCAAGAGTTGAGTACTTGAGAA 420
Qy 421 GAACAAAAGAAATTTATGAGGAGAAATCTTGAATTCGTTGAGCTTGAAGACCTCCAAAG 480
Db 421 GAACAAAAGAAATTTATGAGGAGAAATCTTGAATTCGTTGAGCTTGAAGACCTCCAAAG 480
Qy 481 CTTGAGCATGCTGCTGATGACATCTCAAGCATTTAGGCTAAGAAAGAACCAATCTAT 540
Db 481 CTTGAGCATGCTGCTGATGACATCTCAAGCATTTAGGCTAAGAAAGAACCAATCTAT 540
Qy 541 GTTCGATCATATCTGCGCTCCAGAGAAAGATTAAGCTTGCAAGATCACAAATCTC 600
Db 541 GTTCGATCATATCTGCGCTCCAGAGAAAGATTAAGCTTGCAAGATCACAAATCTC 600
Qy 601 GCTTCTCAAAAAGATTAAAGAGAGAGAGAGAAACGGGTCCAGCAAGAGCAAAATTAGT 660
Db 601 GCTTCTCAAAAAGATTAAAGAGAGAGAGAGAAACGGGTCCAGCAAGAGCAAAATTAGT 660
Qy 661 CCAATGCTCAACTCTCTTCTCAAGTTCTTCTGCTCAATACCTCGTAACCTCTCCAGAGA 720
Db 661 CCAATGCTCAACTCTCTTCTCAAGTTCTTCTGCTCAATACCTCGTAACCTCTCCAGAGA 720
Qy 721 TGGCTTTGGAGAGAGTTGGGGGAGAGAACGGTGTGATGCTGTTGAGCGAAACCAA 780
Db 721 TGGCTTTGGAGAGAGTTGGGGGAGAGAACGGTGTGATGCTGTTGAGCGAAACCAA 780
Qy 781 CTCTGCTTCCGGCTGGATGTACGTCCTACCACTAGAGAGATAGATATCTCTAC 840
Db 781 CTCTGCTTCCGGCTGGATGTACGTCCTACCACTAGAGAGATAGATATCTCTAC 840
Qy 841 TCTTTAATATATATATATATATATATATATATATATATATATATATATATATATAT 900
Db 841 TCTTTAATATATATATATATATATATATATATATATATATATATATATATATATAT 900
Qy 901 TTTGGGACTTATCTCATTTATTAATACGATATGTTAGTAGTACATATATATATAT 960
Db 901 TTTGGGACTTATCTCATTTATTAATACGATATGTTAGTAGTACATATATATATATAT 960
Qy 961 GATGAGACTCCGTTGTCGAGAGATGTACGTAAGCTATCATTAATTCACGCTCTTA 1020
Db 961 GATGAGACTCCGTTGTCGAGAGATGTACGTAAGCTATCATTAATTCACGCTCTTA 1020
Qy 1021 AGAACAAAGATTCATATCTTGTTAATGATTTCTCATGAATA 1062
Db 1021 AGAACAAAGATTCATATCTTGTTAATGATTTCTCATGAATA 1062

RESULT 6
US-09-853-450-3
; Sequence 3, Application US/09853450
; Publication No. US20020194645a1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Brassica oleracea
; FEATURE:
; NAME/KEY: CDS
```

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; LOCATION: (36)..(794)
; OTHER INFORMATION: APETALAI (Ap1)
US-09-853-450-3
Query Match 28.3%; Score 301; DB 9; Length 794;
Best Local Similarity 68.2%; Pred. No. 7, 6e-69;
Matches 418; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

Qy 85 TTGAAGAGAGAGATATGGGAAGAGTAGGGTTGACGTGGAAGAGATGAGAACAAAGT 144
Db 20 TTTAAAGGAGATAAATGGGAGGAGGGGTGCTGAGTGAAGAGAGATGAGAAACAAAGT 79
Qy 145 CATAGAGCAAGTTACTTCTTCAAGAGAGAGTCTGTTGCTGCAAGAGAGCTCATAGAT 204
Db 80 CATAGACAGAGTACATTTCTGCAAGAGAGAGTCTGTTGCTGCAAGAGAGCTCATAGAT 139
Qy 205 CTCTGTTCTGCTGATGCTGAGGTTGCTGCTCATGCTTCTCTTCCAAAGGCAAACTCTT 264
Db 140 CTCTGTTCTGCTGATGCTGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199
Qy 265 CCAATATTTCCACCGACTCTTTCGATGAGAGAGATCTTGAACGCTATGATTCATTTA 324
Db 200 TGAATATCTCAGTATGTTGATGAGAGAGATCTTGAACGCTATGAGAGATCTCTTA 259
Qy 325 TTCAGACAAACAACTGTTGGCCGAGACGTTTCACAAAGTGAAGAAATTTGGTTCTAGACA 384
Db 260 CCGCGAGACAGACTTATATGACACTGATCCGACTCCATACGAACTGTCATGAGAGTA 319
Qy 385 TGTATAGCTCAAGGCAAGAGTTGAGTACTTGAAGAGAAACAAAGAGATTTATGGGGA 444
Db 320 TATATAGGCTTAAGGCTTAAGATTTAGAGTTTGGAGAGAAACAGAGGCACTATCTGGGA 379
Qy 445 ACATCTTGATTTGTTGAGCTTGAAGAGAGTCCAAAGCTTGAAGATCAGCTGATCAGC 504
Db 380 AGACTTGCAGAGAAATGAGCCCTTAAGGAACTCGAATCTAGAGCAACACTGATCTGCG 439
Qy 505 TATCAAGACATTTAGTCAAGAAAGCAAGAGTATGTCGATTCATCTGCTGCTGCA 564
Db 440 TCTTAAGCATTCGCTCTAGAGAAACCACTTATGACACTCCATCATGATAGCTTCCA 499
Qy 565 GAAGAGATTAAGGCTTGCAGAGATCAACAAATTCGCTTCCAAAGATTAAGAGAG 624
Db 500 AAGAAAGGAGAAAGCATACAGGAAACAAACAGACATCTTCCAAACAGATTAAGAGAG 559
Qy 625 GGAGAGAAAGAGGCTACAGCAAGAGAGATTAATGTCATGCTCCAACTCTTCTCAGT 684
Db 560 GGAAGAGGTTCTTAGGGCCCAACAGAGCAATGGAGAGAGAACCATGGCCATTAAT 619
Qy 685 TCTTGCCTCAA 697
Db 620 GCCTCGCCTCCA 632

RESULT 7
US-09-853-450-1
; Sequence 1, Application US/09853450
; Publication No. US20020194645a1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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; NAME/KEY: modified_base
; LOCATION: (778)..(779)
; OTHER INFORMATION: n = g, a, c or t
US-09-853-450-9
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Query Match      25.0%; Score 266; DB 9; Length 779;
Best Local Similarity 69.5%; Pred. No. 9,5e-60;
Matches 378; Conservative 0; Mismatches 160; Indels 6; Gaps 1;
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OY 95 AAGATATGAGGAGAGTGGGTTGAGCTGAGAGAGATGAGAAAGATGCAATGAGCAA 154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4 AAGAGAAATGGGAAGGAGGAGGTTGATGATGAGAGATGAGAAAGATGCAATGAGCAA 63
OY 155 GTTACTTTCTCAAGAGAAGGTGTTGCTCAAGAAAGCTCATGAGATCTCTGTC 214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 64 GTGACATTTCTGAAAAGAAAGAACTGCTTTGGAAGAAAGCTCAGAGATCTCTGTTCTT 123
OY 215 TGGCATGCTGAGGTTGCTCTCATGCTTCTCTTCCAAAGGCAAACTCTTCGAATATTTCC 274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 124 TGTGATGCCGAGGTTCCCTTATGTGCTTCCCAATTAAGGCAAAATGTTGAGTACITCC 183
OY 275 ACCGACTCTGATGAGAGAGATCTGAGACGCTATGATCGCTATTTATTTACAGACAA 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 184 TCTGATCTTGCATGAGAGAGTACTAGAACGCTACGAGAGGATTTCTTACCGCAGAGA 243
OY 335 CAACCTGTTGGCCGAGACGTTTCCAAAGTGAA-----AATTGGGTTCTAGACATGCT 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 244 CAGCTGATTTGACCTGACTCTACGTTAATGCAACAGACAGACTGCTCAATGAGATGAGC 303
OY 389 AAGCTCAAGGCAAGATGAGTACTTGAAGAAACAAAGAAATTTATGAGGGGAGAT 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 304 AGGCTTAAGGCCAAGATTGAGCTTTGGAGAGAAACAAAGCAATATCTGGAGAGAG 363
OY 449 CTGATTTGCTGAGTGTGAGAGAGCTCCAAAGCTTGGAGATCAGCTCAGCTATC 508
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 364 TTGGAAACCAATGAGCTCAAGGATCTCCAAATCTGAGACACACTGAGATCTCTCTT 423
OY 509 AAGACATTAGTCAAGAAAGAACCAAGCTATGTCGAATTCATATCTGCTCCAGAG 568
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 424 AAGCAATTTGCTCCAGAAAAAATCAACATGATGATCCCTCAACCACTCCAAAGA 483
OY 569 AAGATTAAGCCTTCAGAGATCACAACAATTCGCTTCTCAAAAAGATTGAAGAGAGGAG 628
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 484 AAGGAGAGAGAGATACAGAGAGAAAAACAGCATGCTTACCAACAGATTAAGAGAGAGGGA 543
OY 629 AAGA 632
    |||||
DB 544 AACA 547
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RESULT 10
US-09-853-450-7
; Sequence 7, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (149)..(970)
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; OTHER INFORMATION: APELAL1 (Apl)
US-09-853-450-7
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Query Match      24.1%; Score 255.8; DB 9; Length 1345;
Best Local Similarity 67.6%; Pred. No. 5,4e-57;
Matches 359; Conservative 0; Mismatches 172; Indels 0; Gaps 0;
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OY 101 ATGGGAGAGGATGAGGTTGAGCTGAAAGAGATGAGAAACAGATCAATGAGCAAGTACT 160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 149 ATGGGGCCGGCAAGGTACAGCTGAAGCGATGAGAAAGATTAACCGCGAGTGACC 208
OY 161 TTCTCAAGAGAAGATCTGTTGCTCAAGAAAGCTCATGAGATCTCTGTCGAT 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 209 TTCTCAAGCGCGGAGAGCGCTGCTCAAGAGGGCAGAGATCTCGCTCGCTCGAT 268
OY 221 GCTGAGTTGCTCTCATGCTCTTCTCTTCCAAAGGCAAACTCTTGAATATTCACGAC 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 269 GCCGAGGTCGCGCTCATCTCTTCCCAAGGGCAAGCTCTACGATGAGCCACGAC 328
OY 281 TCTTGATGAGAGGATTTGATGAGCTATGATCGCTATTTATTCAGACAAACAACT 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 329 TCCCGCATGACAAATTTCTGACGCTATGAGCGATTTCTATGCTGAAAAGGCTCTT 388
OY 341 GTTGGCCGAGAGCTTTCACAAAGTGAAATTTGGTTCTAGAACATGCTAAGCTCAAGCA 400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 389 ATTTACGCTGATCTGAAGATGAGGGAATTTGGTCCAGAGATACAGAAACTGAAGGCC 448
OY 401 AAGATTGAGTACTTGAGAGAAACAAAGAAATTTATGAGGGAGATCTTGATTCCTTG 460
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 449 AAAATGAGAACCATCAAAATATGCCAAGCACCTGATGGAGAGGATCTAGAGTCTTG 508
OY 461 AGCTTGAAGAGCTCCAAAGCTTGGAGCATGACGCTGATGAGCAAGCTATCAAGACATTAAG 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 509 AATCCCAAGAGCTCCAGACACTAGAGCAGAGCTGATGACTACTGAGAGCAATCAACA 568
OY 521 TCAAGAAAGCAAGAGCTATGTTGATTCATATCTGCTCCAGAGAGATTAAGCC 580
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 569 TCAAGGAAGAGCAGACTTATGAGCGAGCTATTTCTGAGACTACAGAGAGAGAGAGCTA 628
OY 581 TTGCAAGATCACACAAATTCGCTTCTCAAAAAGATTGAAGAGAGGAGAG 631
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 629 CTGCAAGAGAGAGCAAGGCTCTGCAAGAGGAAGATTGGCAGAGAGCGAAG 679
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```
RESULT 11
US-09-853-450-13
; Sequence 13, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Brassica oleracea var. botrytis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(453)
; OTHER INFORMATION: CAULIFLOWER
US-09-853-450-13

Query Match      23.8%; Score 252.6; DB 9; Length 756;
Best Local Similarity 66.6%; Pred. No. 2,8e-56;
Matches 379; Conservative 0; Mismatches 184; Indels 6; Gaps 1;
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```
OY 101 ATGGAGAGAGTGGTTCAGCTGAGAGATAGAGAAACAGATCAATAGGCAAGTTACT 160
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1 ATGGGAAGGGGTAGGGTTGAAATGAAAGAGATAGAGAAACAGATCAACAGACAGTGACG 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 161 TTCTCAAGAGAGAGCTGGTTGGCTCAAGAAAGCTATGAGATCTGTCTCTGCGAT 220
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 61 TTTTCGAAAAGAGAGCTGGCTTTTGAAGAAAGCCCATGAGATCTGATTTCTTGAT 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 221 GCTGAGTTGCTCTCATCGCTTCTCTTCCAAAGGCAAACTCTGATATTTCCACCGAC 280
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 121 GCTGAGTTTCCCTTATTTGCTTCTCTCCATTAAGGGAAACTGTTCGAGTACTGCTGAA 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 281 TCTTGATGAGAGAGTACTTGAACGCTATGATCGTATTTATATTCAGACAAACACTT 340
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 181 TCTTGATGAGAGAGTACTGAGAACGCTACGAGAGTACTTACGCCGGAACAGCTA 240
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 341 GTTGGCGGAGAGCTTTCACAAAGTGA-----AATTGGGTTTACGAACATGCTAACCTC 394
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 241 AAGGCTCAGAGCTCTACGCTCAATGCACAAAGCAAGTGTCAATGGAATATAGCAGGCTT 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 395 AAGGCAAGAGTTGAGTACTTGAAGAGAACAAAGCAATTTATGGGGAGATCTTGAT 454
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 301 AAGGCTAAGATTGAGCTTTGGAGAGAGAACCAAGCATTTATCTGGAGAGAGATTAGAA 360
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 455 TCGTTGAGCTTGAAGAGCTCCAAAGCTTGAGCAGTCTGATGAGCTATCAAGAGC 514
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 361 TCAATCAGCATTAAGAGAGTACAGAAATCTGAGCAGAGCTTGACACTTCTTTAAACAT 420
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 515 ATTAGTCAAGAAAGAACCAAGTATGTTGATTCATATCTGGCTCCAGAGAGAGAT 574
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 421 ATTGCTCGAAGAAATACTAATGCACTAGTCCCTCAACCACTCCAAAGAGAG 480
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 575 AAGGCTTGCAGAGATCAACAATTCGCTTCTCAAAAAGATTAAAGAGAGAGAGAA 634
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 481 AAGAATAATCTGGAGAGAAACAGCATGCTTGCCAAACAGATTAAGAGAGAGATATC 540
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 635 ACGGCTCAGCAAGAGAGACATTAGTCCA 663
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 541 CTAAGGACACATCAAAACCAATCAGAGCA 569
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

```
RESULT 12
US-09-853-450-11
; Sequence 11, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Brassica oleracea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(756)
; OTHER INFORMATION: CAULIFLOWER
US-09-853-450-11
```

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Query Match 23.3%; Score 247.8; DB 9; Length 756;
Best Local Similarity 66.1%; Pred. No. 5e-55;
Matches 376; Conservative 0; Mismatches 187; Indels 6; Gaps 1;
```

QY 101 ATGGAGAGAGTGGTTCAGCTGAGAGATAGAGAAACAGATCAATAGGCAAGTTACT 160

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||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 1 ATGGGAAGGGGTAGGGTTGAAATGAAAGAGATAGAGAAACAGATCAACCGAAGTGACG 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 161 TTCTCAAGAGAGAGCTGGTTGGCTCAAGAAAGCTATGAGATCTGTCTCTGCGAT 220
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 61 TTTTCGAAAAGAGAGCTGGCTTTTGAAGAAAGCCCATGAGATCTGATTTCTTGAT 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 221 GCTGAGTTGCTCTCATCGCTTCTCTTCCAAAGGCAAACTCTGATATTTCCACCGAC 280
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 121 GCTGAGTTTCCCTTATTTGCTTCTCTCCATTAAGGGAAACTGTTCGAGTACTGCTGAA 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 281 TCTTGATGAGAGAGTACTTGAACGCTATGATCGTATTTATATTCAGACAAACACTT 340
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 181 TCTTGATGAGAGAGTACTGAGAACGCTACGAGAGTACTTACGCCGGAACAGCTA 240
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 341 GTTGGCGGAGAGCTTTCACAAAGTGA-----AATTGGGTTTACGAACATGCTAACCTC 394
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 241 AAGGCTCAGAGCTCTACGCTCAATGCACAAAGCAAGTGTCAATGGAATATAGCAGGCTT 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 395 AAGGCAAGAGTTGAGTACTTGAAGAGAACAAAGCAATTTATGGGGAGATCTTGAT 454
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 301 AAGGCTAAGATTGAGCTTTGGAGAGAGAACCAAGCATTTATCTGGGCGAAGTTAGAA 360
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 455 TCGTTGAGCTTGAAGAGCTCCAAAGCTTGAGCAGTCTGATGAGCTATCAAGAGC 514
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 361 TCAATCAGCATTAAGAGAGTACAGAAATCTGAGCAGAGCTTGACACTTCTTTAAACAT 420
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 515 ATTAGTCAAGAAAGAACCAAGTATGTTGATTCATATCTGGCTCCAGAGAGAGAT 574
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 421 ATTGCTCGAAGAAATACTAATGCACTAGTCCCTCAACCACTCCAAAGAGAG 480
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 575 AAGGCTTGCAGAGATCAACAATTCGCTTCTCAAAAAGATTAAAGAGAGAGAGAA 634
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 481 AAGAATAATCTGGAGAGAAACAGCATGCTTGCCAAACAGATTAAGAGAGAGATATC 540
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY 635 ACGGCTCAGCAAGAGAGACATTAGTCCA 663
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 541 CTAAGGACACATCAAAACCAATCAGAGCA 569
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

```
RESULT 13
US-09-938-842a-3474
; Sequence 3474, Application US/0938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3474
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842a-3474
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Query Match 21.7%; Score 230; DB 9; Length 1241;
Best Local Similarity 100.0%; Pred. No. 2.7e-50;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 830 AACTATCTACCTCTTATATATATGATTAATTAATTAATGTTTAATTAATTTTCATAACA 889



Db 421 TGCATCAAGACACGATATATGCTTGACCAAGCTCTCTGATCTTCAAGGTAAGGACATATC 480  
Oy 581 TTGCAAGATCACAACAATTGCTTCTCAAAAAGATTAAAGAGAG 625  
||| ||| ||| | | | | | | | | | |  
Db 481 TTGCTTGATGCCAACAAGAGCTTTGTCAATGAGCTGGAAGATATG 525

Search completed: February 2, 2003, 05:41:08  
Job time : 98 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 2, 2003, 05:41:13 ; Search time 2182 Seconds  
(without alignments)  
7882.496 Million cell updates/sec

Title: US-09-981-087A-1

Perfect score: 1062

Sequence: 1 ccagagagacataagaag.....taatgatttcctatgaata 1062

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estbun:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estrov:\*  
6: em\_estrpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	682.4	64.3	685	10	AV822813
2	435	41.0	455	10	AV794470
3	358.8	33.8	362	10	AV563010
4	350	33.0	396	10	AV817219
5	327.4	30.8	680	14	BQ148488
6	327.2	30.8	951	12	BG838400

7	316	29.8	777	10	BE034098
8	313.2	29.5	637	10	AM442341
9	313.2	29.5	729	10	AM442282
10	310.2	29.2	610	10	AM441624
11	310.2	29.2	640	13	BI930479
12	310.2	29.2	682	9	AI486645
13	308.8	29.1	653	10	AM930971
14	308.6	29.1	638	13	BM411808
15	305	28.7	634	10	AM441346
16	303.8	28.6	588	10	BE431620
17	302.8	28.5	639	10	AM223473
18	302	28.4	728	13	BM412293
19	301.2	28.4	535	9	AI489508
20	301	28.3	559	10	BE460489
21	301	28.3	618	13	BM535331
22	301	28.3	763	13	BM412720
23	297.8	28.0	560	10	AM222435
24	297.8	28.0	675	12	BG888499
25	297.8	28.0	782	14	BQ510995
26	297.4	28.0	515	10	BE435803
27	296	27.9	528	10	AM220728
28	292.4	27.5	613	13	BM406322
29	291.8	27.5	534	9	AI4898519
30	287.8	27.1	507	10	AM222490
31	286.8	27.0	514	10	AM930435
32	276.8	26.1	488	12	BE052183
33	275.6	26.0	755	14	BQ988395
34	274.6	25.9	654	14	BQ010049
35	273	25.7	739	14	BQ986698
36	268.6	25.3	541	10	AM931475
37	268	25.2	548	10	AM932141
38	266.2	25.1	574	10	AM931861
39	264	24.9	638	9	AU236519
40	262.6	24.7	470	10	BE436562
41	262.6	24.7	495	10	AM254887
42	262	24.7	586	14	BQ454007
43	260.8	24.6	517	10	AM441991
44	260.4	24.5	581	9	AI487956
45	256.6	24.2	438	14	BQ149729

## ALIGNMENTS

RESULT 1  
LOCUS AV822813 685 bp mRNA linear EST 01-APR-2002  
DEFINITION AV822813 RAPUS Arabidopsis thaliana cDNA clone RAFU05-11-024 5',  
mRNA sequence.  
ACCESSION AV822813  
VERSION AV822813.1 GI:19864865  
KEYWORDS  
SOURCE  
ORGANISM  
thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
1 (bases 1 to 685)  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Araoka, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
and Shinozaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel.: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rct.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al., 1998). This clone is in a

modified pBluescript vector as a SstI/XhoI insert. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

FEATURES	Location/Qualifiers
source	1. .685

dehydration-treated(1,2,5,10,24 hr)"

Query Match	64.3%	Score 682.4	DB 10	Length 685
Best Local Similarity	99.7%	Pred. No. 1.2e-160		
Matches 683	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

QY	39	TTTGGCATTTTACGGGTTTCGTTTCCTCTCTCTGTGTTCTTGAGATTTTAAAGAGACAG	98
Db	1	TTGGGTCATTTTACGGGTTTCGTTTCCTCTCTCTGTGTTCTTGAGATTTTAAAGAGAGAG	60
QY	99	ATATGGAAGAGAGTATGGGTTTCAGCTGTAAGAGATAGAGAACAAGATCAATATAGGCAAGTAA	158
Db	61	ATATGGAAGAGAGTATGGGTTTCAGCTGTAAGAGATAGAGAACAAGATCAATATAGGCAAGTAA	120
QY	159	CTTTCCTCAAGGAAGAGCTGTGGTTTGGTCTCTCAAGAAAGCTATAGATCTCTGTCTCTGG	218
Db	121	CTTTCCTCAAGGAAGAGCTGTGGTTTGGTCTCTCAAGAAAGCTATAGATCTCTGTCTCTGG	180
QY	219	ATGCTGAGGTTTCCTCATCGTCTCTCTCTCTCCAAAGGCAAACTCTTCGAATATTCACACG	278
Db	181	ATGCTGAGGTTTCCTCATCGTCTCTCTCTCTCCAAAGGCAAACTCTTCGAATATTCACACG	240
QY	279	ACTCTTCGATGAGAGAGATCTTGAACGCTATGATCGCTATTTATATTTAGACAAACAC	338
Db	241	ACTCTTCGATGAGAGAGATCTTGAACGCTATGATCGCTATTTATATTTAGACAAACAC	300
QY	339	TTGTTTGGCCGAGACCTTTCACAAAGTGAATAATTTGGGTTTATAGACATGCTTAAGCTCAAG	398
Db	301	TTGTTTGGCCGAGACCTTTCACAAAGTGAATAATTTGGGTTTATAGACATGCTTAAGCTCAAG	360
QY	399	CAAGGTTGAGTACTTGAAGAAGAACAAAGGAATTTTATGGGGGAAGATCTTGATTGCT	458
Db	361	CAAGGTTGAGTACTTGAAGAAGAACAAAGGAATTTTATGGGGGAAGATCTTGATTGCT	420
QY	459	TGAGCTTCAAGAGAGCTCCAAAGCTTGGAGACATCAGCTGCATCAGTATCAAGACATTA	518
Db	421	TGAGCTTCAAGAGAGCTCCAAAGCTTGGAGACATCAGCTGCATCAGTATCAAGACATTA	480
QY	519	GGTCAAGAAAGAACCAAGCTATGTTGCAATTCATATCTGCGCTCCAGAAAGAGATTAAAG	578
Db	481	GGTCAAGAAAGAACCAAGCTATGTTGCAATTCATATCTGCGCTCCAGAAAGAGATTAAAG	540
QY	579	CCTTCACAGATCACAAACATTCGCTTCTCCAAAATAATTAAGAGAGGGAAGAAACAGG	638
Db	541	CCTTCACAGATCACAAACATTCGCTTCTCCAAAATAATTAAGAGAGGGAAGAAACAGG	600
QY	639	GTCAGCAAGAGAGCAATATAGTCCAATCTCCACATCTCTTCACATCTCTGCGCTCAAT	698
Db	601	GTCAGCAAGAGAGCAATATAGTCCAATCTCCACATCTCTTCACATCTCTGCGCTCAAT	660
QY	699	ACTGCGTAACCTCCTCCACAGATGG	723
Db	661	ACTGCGTAACCTCCTCCACAGATGG	685

RESULT 2	LOCUS	DEFINITION
AV794470/c	455 bp	mrna
AV794470	linear	EST 29-MAR-2002
AV794470	RAFL8	Arabidopsis thaliana CDNA clone RAFL08-13-A09 3'

ACCESSION	AV794470	
VERSION	AV794470.1	GI:19828453
KEYWORDS	EST.	
SOURCE	thale cress.	

ORGANISM

thale cress.  
*Arabidopsis thaliana*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 455)

**AUTHORS**  
Seki, M., Nurusaka, M., Ishida, J., Kamuya, A., Satou, M., Nakajima, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashida, K., and Shinozaki, K.

**TITLE**  
Large scale analysis of Arabidopsis full-length cDNA (2002b)

**RECEIVED**  
Received 10/20/2002

FEATURES	Location/Qualifiers
source	1. .455

BASE COUNT	150 a	87 c	85 g	133 t
ORIGIN				

Query Match	41.0%;	Score 435;	DB 10;	Length 455;
Best Local Similarity	100.0%;	Pred. No. 1.4e-98;		
Matches 435; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

[illegible]



QY	926	TACCATATGTTTGGCTGTCATATTTAATGATGAGCACTCGTGTGAGACGTA	985
Db	157	TACCATATGTTTGGCTGTCATATTTAATGATGAGCACTCGTGTGAGACGTA	99
QY	986	TGTAGTAAGCTATCATTTAGATTCACTGCGCTTAAGAACAAAGATTATATCTTGTTAA	1045
Db	98	TGTAGTAAGCTATCATTTAGATTCACTGCGCTTAAGAACAAAGATTATATCTTGTTAA	39
QY	1046	TGATTTCTCATGAA	1059
Db	38	TGATTTCTCATGAA	25
RESULT 5			
LOCUS	B0148488	680 bp	linear
DEFINITION	MF068H07FL11064	Developing flower	Medicago truncatula cDNA clone
ACCESSION	B0148488		
VERSION	B0148488.1	GI:20285547	
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
REFERENCE	1 (bases 1 to 680)		
AUTHORS	Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,...		
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: May GD Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380 Email: gdmay@noble.org Insert Length: 680 Std Error: 0.00 Plate: 068 row: H column: 07 Seq primer: TCACACAGGAACACGCTATGAC. Location/Qualifiers 1..680 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF068H07FL" /clone_lib="Developing flower" /tissue_type="Developing flowers" /dev_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods." /note="Vector: Lambda Zap; cDNA was prepared from polyA+ RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XL1-blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."		
BASE COUNT	247 a	110 c	134 g
ORIGIN			184 t
Query Match	30.8%	Score 327.4	DB 14: Length 680;
Best Local Similarity	75.6%	Pred. No. 1.5e-71	
Matches 403; Conservative	0;	Mismatches 130;	Indels 0; Gaps 0;
101 ATGGAGAAAGGTAGGCTTCACCTGAAGAGATAGAACAAAGATCATATAGCACTTACT	160		

Db	Accession	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	130	ATGGGAGGGGAAAGAGTGCAGTGAAGAGCATTGGAACCAAGATCAATPAGCAAGTCAC	189										
Qy	161	TTTCTCAAGAGGAAGGTCTGGTTGCTCAAGAAAGCTCATGAGATCTCTGTTCTCTGGCAT	220										
Db	190	TTTTTCAAGAGGAAGGTCTGGTTGTTGGAAGAAAGCAAGCAAGATCTCTGTTCTTGTGAT	249										
Qy	221	GCTAGATCTCTCATCGTCTCTCTTCGCAAGGCAAACTCTTCGAAATATTCACGAC	280										
Db	250	GCTAAATTTGCTCTCATATTTTCTCTCTACTAAAGCAAGCTTTTGAATCTCAGAGAT	309										
Qy	281	TCCTTGATGAGAGGATCTTGAGCGCTATGATGCGCTATATATATTCAGACAAACAATT	340										
Db	310	CCTTGATGAGAAAAAATCTTGAAACGATATGAAAGATGTCGTATATGAGAGGCAACTT	369										
Qy	341	GTTGGCGGACAGCTTTCACAAAGTGAAATTTGGTTCTAGAACATGCTAAGCTCAAGCA	400										
Db	370	GTTCAAGTACAGACATCACCAATGAAATTTGGTTCTAGAGCACCGAANAATCTAAGCT	429										
Qy	401	AGAGTTGAGGTACTGTGAGAAAGCAAAAGAAATTTATGGGGGGAAGATCTTGTGTTG	460										
Db	430	AGATATGAGATGCTCTCAGAGAAATCAAAAGAAATTTATGGGAAAGACTTGATGTTTA	489										
Qy	461	AGCTTGAGAGAGCTCCAAAGCTTGGAGACTACGCTCGATGCACTATCAAGACATTAG	520										
Db	490	NGTCTCAAAAGGTTCAAAAGTTGGAAACAACTTGAATTAGCTTCACAAACAAATTAGA	549										
Qy	521	TCAGAAGAAGCAACAGCTATGTTGCAATCATATCGGCTCCAGAGAAGCATTAAGCC	580										
Db	550	TCACGGAAGAACCAAGTATGTAATGATCTATTTCAANAATCTTCANAAAAAGATTAAGCC	609										
Qy	581	TTGCAAGATCAACAACATTCGCTTCTCAAAAAGATTAAGAGAGGAGAGAA	633										
Db	610	CTNCAGAACATATACAAACATGCTACCAAGAGATTAAGGAAAGAGAGGA	662										
RESULT 6	BG838400			BG838400									
LOCUS	BG838400	951 bp	mRNA										
DEFINITION	Gc01_02c02_A Gc01_AAFRC_ECORC_cold_stressed_glycine_clandestina												
ACCESSION	BG838400												
VERSION	BG838400.1	GI:14204722											
KEYWORDS	EST.												
SOURCE	Glycine clandestina.												
ORGANISM	Glycine clandestina												
REFERENCE	1 (Phases 1 to 951)												
AUTHORS	Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris												
	,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker												
	,N.A.												
TITLE	Expressed sequence tags from Cold-Stressed Glycine clandestina												
JOURNAL	Unpublished (2001)												
COMMENT	Contact: Singh,J.A.												
	Eastern Cereal and Oilseed Research Centre												
	Agriculture and Agri-food Canada												
	KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A												
	O6, Canada												
	Tel: (613) 759-1662												
	Fax: (613) 759-1701												
	Email: singhja@em.agr.ca.												

/tissue\_type="Leaves, stem"  
 /note="Vector: Bluescript SK+/XhoI-EcoRI; Site\_1: EcoRI; Site\_2: XhoI; Plants incubated at 2 degrees under 12 hours of light/day. Harvested after only 2-3 days of cold treatment. cDNA was prepared with the Uni-Zap cDNA kit from Stratagene. Eco RI adapters were linked followed by digest with Xho I/Eco RI and ligated to pluescript."  
 BASE COUNT 313 a 179 c 214 g 245 t  
 ORIGIN

Query Match 30.8%; Score 327.2; DB 12; Length 951;  
 Best Local Similarity 72.3%; Pred. No. 1.8e-71;  
 Matches 425; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 77 TTGATTTTGAAGAGAGATATGGAGAGAGAGAGAGAGAGATAG 136  
 DB 36 TTGATTTTGAAGAGATATATATGGAGAGAGAGAGAGAGATAG 95  
 QY 137 AACAGATCAATAGGCAAGTACTTCTCAAGAGAGAGAGAGAGAG 196  
 DB 96 AACAGATCAATAGGCAAGTACTTCTCAAGAGAGAGAGAGAGAG 155  
 QY 197 CATGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 256  
 DB 156 CGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 215  
 QY 257 AAACCTTGAATATTCACACGACTCTTGCATGGAGAGAGATGATGC 316  
 DB 216 AACCTTTCGACTCTGCAAGACCTTGTATGAAAGAAATTTGAACT 275  
 QY 317 TATTTATTCAGAAACAACTTGTGGCGAGAGAGAGAGAGAGAGAG 376  
 DB 276 TATTTATTCAGAAACAACTTGTGGCGAGAGAGAGAGAGAGAGAG 335  
 QY 377 CTAGAATCTGTAACCTCAAGCAAGAGTGGAGTACTTGAAGAAAG 436  
 DB 336 ATGGAACACGAAAGAGCTTAAGAGTGGAGTGGAGTGGAGTGGAG 395  
 QY 437 ATGGGGAAGATCTTGATGCTTGAAGAGCTTCAAGAGTGGAGTGGAG 496  
 DB 396 ATGGGGAAGATCTTGATGCTTGAAGAGCTTCAAGAGTGGAGTGGAG 455  
 QY 497 GATGAGCTATCAAGACATTAAGTCAAGAGAGAGAGAGAGAGAGAT 556  
 DB 456 GATTCCTCTCAAAACATTAATATCAACAAAGAGAGAGAGAGAGAT 515  
 QY 557 GCGCTCAGAGAGAGATTAAGCTTGCAGAGATCAACAAATTCCTCT 616  
 DB 516 GCGCTCAGAGAGAGATTAAGCTTGCAGAGATCAACAAATTCCTCT 575  
 QY 617 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664  
 DB 576 AAGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 623

RESULT 7  
 BE034098 777 bp mRNA linear EST 07-JUN-2000  
 LOCUS  
 DEFINITION MG03B05 MG Mesembryanthemum crystallinum  
 maas-box protein, mRNA sequence.  
 ACCESSION BE034098  
 VERSION BE034098.1 GI:8329107  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Mesembryanthemum crystallinum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Caryophyllales; Alzooceae; Mesembryanthemum.  
 Bohnert.H.J., Borchert.C., Brazille.S., Brooks.J., Eaton.M., Ferreira  
 Scara.G., Wheeler.M., McColough.A., Michalowski.C.B., Palacio.C.,  
 Functional Genomics of Plant Stress Tolerance

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Michalowski,C.B.  
 University of Arizona  
 Bio Sciences West room 513, Tucson, AZ 85721, USA  
 TEL: 520-621-7982  
 FAX: 520-621-1697  
 Email: chmeh@arizona.edu

## FEATURES

source

Location/Qualifiers  
 1..777  
 /organism="Mesembryanthemum crystallinum"  
 /db\_xref="taxon:3544"  
 /clone\_lib="MG"  
 /tissue\_type="roots"  
 /dev\_stage="5-6 weeks"  
 /note="grown in hydroponics, stress 400 mM NaCl (in 0.5 Hoagland's), 30 h stress"

## BASE COUNT

250 a 155 c 198 g 172 t 2 others

## Query Match

Best Local Similarity 29.8%; Score 316; DB 10; Length 777;  
 Matches 415; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 87 GAAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGATCA 146  
 DB 77 GAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCA 136  
 QY 147 ATAGCAGAGATCTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 206  
 DB 137 ACCGTGAGATCTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 196  
 QY 207 CTGTTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 266  
 DB 197 CTGTTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 256  
 QY 267 AATTTTCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 326  
 DB 257 AGTAGCTTTGATGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 316  
 QY 327 CAGACAAACAACTTGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 386  
 DB 317 CAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 376  
 QY 387 CTAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 446  
 DB 377 CAAAGCTCAAGGCTAGGCTGAGAAATCTTCAAGAAATCAAGGATTA 436  
 QY 447 ATCTGATTCGTTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 506  
 DB 437 AACCTGATTCGTTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAT 496  
 QY 507 TCAAGATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 566  
 DB 497 TTTAAACATATCAAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAT 556  
 QY 567 AGAAGAGATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 626  
 DB 557 AGAAGAGATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 616  
 QY 627 AGAAGAGATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666  
 DB 617 AGAAGAGATTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 656

## RESULT 8

AW42341

LOCUS

## DEFINITION

EST11737 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA

## ACCESSION

AW42341

## VERSION

AW42341.1 GI:6977592

KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 637)  
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,  
Upson,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,  
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.  
Generation of ESTs from tomato fruit tissue  
Unpublished (1999)  
CONTACT: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

FEATURES  
source  
1. .637  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="clEN22N3"  
/clone\_1lb="tomato fruit red ripe, TAMU"  
/tissue\_type="pericarp"  
/dev\_stage="red ripe (7-20 days post-breaker)"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; supplier: Giovannoni; Fruit were tagged at the  
breaker stage (first sign of lycopene accumulation on the  
blossom end of the fruit) and harvested 7 days  
post-breaker (fully red-ripe), 10 days post breaker, and  
20 days post-breaker (over-ripe). 20 day fruit which  
showed external or internal signs of pathogenesis were  
discarded. Fruit were cut in half and the seeds and  
locules were discarded prior to freezing the pericarp."  
Location/Qualifiers  
208 a 120 c 150 g 159 t

BASE COUNT  
ORIGIN

Query Match 29.5%; Score 313.2; DB 10; Length 637;  
Best local Similarity 73.1%; Pred. No. 5.4e-68;  
Matches 402; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

OY 99 ATATGGAAGAGGAGGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 158  
1 AAATGGGAAGAGAGAGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 60  
159 CTTTCTCAAGAGAGAGGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 218  
61 CTTTCTCAAGAGAGAGGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 120  
OY 219 ATGCTGAGGTTCCTCTGCTCTCTCTCAAGAGCAAGCTCTGATATTCACAGC 278  
121 ATGCTGAGGTTCCTCTGCTCTCTCTCAAGAGCAAGCTCTGATATTCACAGC 180  
Db 121 ATGCTGAGGTTCCTCTGCTCTCTCTCAAGAGCAAGCTCTGATATTCACAGC 338  
OY 279 ACTCTTGATGAGAGAGATCTGATGAGCTATGATCCCTATTTTATTCAGACAAAC 338  
101 ATCTCTGATGAGAGAGATCTGATGAGCTATGATCCCTATTTTATTCAGACAAAC 240  
Db 101 ATCTCTGATGAGAGAGATCTGATGAGCTATGATCCCTATTTTATTCAGACAAAC 398  
OY 339 TTGTTGGCCGAGAGCTTCACAAAGTGGGTTCTAGACATGCTAGGCTAGG 398  
101 TTGTTGGCCGAGAGCTTCACAAAGTGGGTTCTAGACATGCTAGGCTAGGCTAGG 300  
Db 241 TTGTTGGCCGAGAGCTTCACAAAGTGGGTTCTAGACATGCTAGGCTAGGCTAGG 458  
OY 399 CAAGAGTTGAGTACTTGAAGAGCAAAAGATTTATGGGGAGATCTTATTCGT 458  
101 CAAGAGTTGAGTACTTGAAGAGCAAAAGATTTATGGGGAGATCTTATTCGT 360  
Db 301 CCAGAGTTGAGTACTTGAAGAGCAAAAGATTTATGGGGAGATCTTATTCGT 518  
OY 459 TGAAGCTTGAAGAGCTCCAAAGCTTGAGCATCAGCTGATCCAGCTATCAAGACATTA 518  
101 TGAAGCTTGAAGAGCTCCAAAGCTTGAGCATCAGCTGATCCAGCTATCAAGACATTA 420  
Db 361 TGAAGCTTGAAGAGCTCCAAAGCTTGAGCATCAGCTGATCCAGCTATCAAGACATTA 578  
OY 519 GGTCAAGAAAGAGCAAGCTATGTTGCAATTCATATCTGCGCTCCAGAAAGAGATTAAG 578

Db 421 GATCAAGAAAGAAATCAATGATGATGATGCTCTCTGCTTCAAAAAAGGACAGAG 480  
OY 579 CCTTCAAGATCACACAAATTCGCTTCTCAAAAAAGATTAAGAGAGGAGAAAGAGG 638  
101 CCTTCAAGATCACACAAATTCGCTTCTCTCAAAAAAGATTAAGAGAGGAGAAAGAGG 540  
Db 481 CATTGAGAGAGCAAAACACAGCTTTCGAAGAAGGTGAAGAGAGAGAAAGAGGTGG 540  
OY 639 GTGAGCAAGA 648  
101 GTGAGCAAGA 550  
Db 541 CACAGCAAAA 550

RESULT 9  
AM442282 729 bp mRNA linear EST 18-MAY-2001  
LOCUS EST311678 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA  
DEFINITION  
AM442282  
AM442282  
AM442282.1 GI:6977533  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
tomato.  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 729)  
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,  
Upson,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,  
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.  
Generation of ESTs from tomato fruit tissue  
Unpublished (1999)  
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Clemson University  
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Email: <http://www.genome.clemson.edu/orders/index.html>  
5 prime sequence.

FEATURES  
source  
1. .729  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="clEN22M20"  
/clone\_1lb="tomato fruit red ripe, TAMU"  
/tissue\_type="pericarp"  
/dev\_stage="red ripe (7-20 days post-breaker)"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; supplier: Giovannoni; Fruit were tagged at the  
breaker stage (first sign of lycopene accumulation on the  
blossom end of the fruit) and harvested 7 days  
post-breaker (fully red-ripe), 10 days post breaker, and  
20 days post-breaker (over-ripe). 20 day fruit which  
showed external or internal signs of pathogenesis were  
discarded. Fruit were cut in half and the seeds and  
locules were discarded prior to freezing the pericarp."  
Location/Qualifiers  
240 a 135 c 173 g 181 t

BASE COUNT  
ORIGIN

Query Match 29.5%; Score 313.2; DB 10; Length 729;  
Best local Similarity 73.1%; Pred. No. 5.5e-68;  
Matches 402; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

OY 99 ATATGGAAGAGGAGGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 158  
1 AAATGGGAAGAGAGAGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 61  
Db 2 AAATGGGAAGAGAGAGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 218  
OY 159 CTTTCTCAAGAGAGAGGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 218  
101 CTTTCTCAAGAGAGAGGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 121  
Db 62 CTTTCTCAAGAGAGAGGTTCAGCTGAAGAGATAGAGACAGATCAATAGCAAGTTA 278  
OY 219 ATGCTGAGGTTCCTCTGCTCTCTCTCAAGAGCAAGCTCTGATATTCACAGC 278  
101 ATGCTGAGGTTCCTCTGCTCTCTCTCAAGAGCAAGCTCTGATATTCACAGC 278

```

"/new-stage/red-ripe (/~/20 days post-breaker)"
/next-sector: pbluscript SK (/); Site_1: EORR; Site_2:
/whole-plant: Giovannianni; Fruit were tagged at the
breaker stage; first sign of lycopene accumulation on the
blossom end of the fruit; and harvested 7 days
post-breaker (full, red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were

```

[illegible]



Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
This clone is available through the Clemson University Genomics Institute

FEATURES  
source  
Seq primer: 73.

Location/Qualifiers  
1. 640  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="CTOC16P17"  
/clone.lib="tomato flower, 8 mm to preanthesis buds"  
/tissue\_type="flower"  
/dev\_stage="buds 8mm to preanthesis"  
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research, Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496) they were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

BASE COUNT  
ORIGIN

29.2%; Score 310.2; DB 13; Length 640;  
Best local Similarity 72.4%; Pred. No. 3.1e-67;  
Matches 402; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

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91 AGAGAGATATGGAAGAGGTAGCTTCAGCTGAGAGAGTAGAACAATCAATAG 150
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8 AGAATTAATATGGGTAGAGAGAGATGACATTTAGAGATTAGAACAATAATATCG 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
151 GCAAGTACTTCTCAAGAAGAGCTGCTGTTGCTCAAGAAGCTCATGATCTGT 210
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 TCAAGTTACTTTTCAAGAAGAGCTGCTGTTGCTTAAAGCAAGCTCATGATCTGT 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
211 TCTCGCATCTGAGTCTGCTCATGCTGCTTCTTCAAGCAAGCTCTTGATA 270
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
128 GCTTGGCATCTGAAAGTGAAGTCAATTTTCTCAACCTAAGAAAGCTTTGAGTA 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
271 TTCCACGACTCTTGATGAGAGAGTACTTGAACGCTATGCTATTTATTCAGA 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
188 TTCTACTACTCTTCATGGAAGAGTCTGGAAGGATATGAAGGATCATATGCTGA 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
331 CAACAACCTGTTGCCCGAGAGCTTTCAACAAGTGAAGATGGGTTTCAACAATGCTAA 390
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
248 AAGGAGCTTATGCTACTGATATTAACCCCGGTAGCTGAGCTTTGGAACATGCTAA 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
391 GCTCAAGCAAGTGTGAGTACTTGAAGAACAAGAAAGAAATTTTATGGGGGAAGATCT 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
308 GCTTAAGGCCACATTTGAGGTTTTCAGAAACCAACCAAGCATTTAGCAGAGAGAGCTT 367
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
451 TGATTCGTTGAGCTGAGAGAGCTCCAAAGCTTGAGCATGAGCTGATGAGCTATCA 510
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
368 GGACACATTTAGATGAAGAGCTTCGAATCTGGAACCGAGCTGATTTGCTTTAA 427
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
511 GAGCATTTAGCTCAAGAAACCAAGCTATGTTGCAATTCATATCTGCTCCAGAGAA 570
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
428 GCACATTTGATCTAGAAAGACCAATTTGATGATGATGATTCATTTCTGACCTTCAAGAA 487
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
571 GCATTAAGCTTGAAGATCAACAATTCCTTCTCAAAAAGATTAAAGAGAGAGAA 630
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488 GGACAAAGGATTCAGAAAGCAACAATCTTTCAAGCAGGTTAAGGAAAGGAGAA 547
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
631 GAAACGGGTGACCA 645
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
548 AGAGATGGCCCAACA 562
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RESULT 12  
A1486645 682 bp mRNA linear EST 18-MAY-2001  
A1486645  
LOCUS A1486645 tomato ovary, TAMU Lycopersicon esculentum cDNA clone  
DEFINITION EST244966

CLEED118, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

A1486645  
A1486645.1 GI:4382016  
EST.  
tomato.  
Lycopersicon esculentum  
Lycopersicon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE  
AUTHORS

1 (bases 1 to 682)  
Alcala, J., Vredolov, J., White, R., Matern, A. L., Vision, T., Holt, I. E.,  
Liang, F., Upton, J., Ronning, C. M., Craven, M. B., Fujii, C. Y., Bowman,  
C. L., Nierman, M., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley,  
S. D. and Giovannoni, J.

TITLE  
JOURNAL  
COMMENT

Generation of ESTs from tomato carpel tissue  
Unpublished (1999)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES  
source

1. 682  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="CLEED118"  
/clone.lib="tomato ovary, TAMU"  
/tissue\_type="carpel"  
/dev\_stage="5 days pre-anthesis to 5 days post-anthesis"  
/lab\_host="XLI-Blue MRP"  
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; cLED - Tomato Carpel EST library. OligodT-primed and directionally cloned cDNA in vector Lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

BASE COUNT  
ORIGIN

29.2%; Score 310.2; DB 9; Length 682;  
Best local Similarity 72.4%; Pred. No. 3.1e-67;  
Matches 402; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

```

91 AGAGAGATATGGAAGAGGTAGGCTCAGCTGAGAGAGTAGAACAATCAATAG 150
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
82 AGAATTAATATGGGTAGAGAGAGATGACATTTAGAGATTAGAACAATAATATCG 141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
151 GCAAGTACTTCTCAAGAAGAGCTGCTGTTGCTCAAGAAGCTCATGATCTGT 210
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
142 TCAAGTTACTTTTCAAGAAGGAGTCTGTTGCTTAAAGCAAGCTCATGATCTGT 201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
211 TCTCGCATCTGAGTCTGCTCATGCTGCTTCTTCAAGCAAGCTCTTGATA 270
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
202 GCTTGGCATCTGAAAGTGAAGTCAATTTTCTCAACCTAAGAAAGCTTTGAGTA 261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
271 TTCCACGACTCTTGATGAGAGAGTACTTGAACGCTATGCTATTTATTCAGA 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
262 TTCTACTACTCTTCATGGAAGAGTCTGGAAGGATATGAAGGATCATATGCTGA 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
331 CAACAACCTGTTGCCCGAGAGCTTTCAACAAGTGAAGATGGGTTTCAACAATGCTAA 390
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
322 AAGCAGCTTAAATGCTACTGATATTAACCCCGGTAGCTGAGCTTTGGAACATGCTAA 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
271 GCTCAAGCAAGTGTGAGTACTTGAAGAACAAGAAATTTTATGGGGGAAGATCT 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
382 GCTTAAGGCCACATTTGAGGTTTTCAGAAACCAACCAAGCATTTAGCAGAGAGAGCTT 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
451 TGATTCGTTGAGCTGAGAGAGCTCCAAAGCTTGAGCATGAGCTGATGAGCTATCA 510
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
442 GGACAAAGGATTCAGAAAGCAACAATCTTTCAAGCAGGTTAAGGAAAGGAGAA 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
511 GAGCATTTAGCTCAAGAAACCAAGCTATGTTGCAATTCATATCTGCTCCAGAGAA 570
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```



Db 222 GCTTGGGATGCTGAAGTTGGACTCATTTCTCACTAAAGGAAACTCTTGAGTA 281

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Seq primer13.
Location/Qualifiers
1.638
/organism="Lycopersicon esculentum"
/cultivar="TA436"
/db_xref="taxon:4081"
/clone="CLEG57P12"
/clone.lib="tomato breaker fruit"
/rissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/note="Vector: pBluescriptSKmCunadapl; site_1: EcoRI;
site_2: XhoI; supplier: Boyce Thompson Institute; Fruit
sequencing: The Institute for Genomic Research. Fruit
were harvested at the blossom stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded

```

